

SEQUENCE LISTING

<110> DIVERSA CORPORATION
 LAM, David
 MATHUR, Eric

<120> ENDOGLUCANASES

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<140> 09/914,543

<141> 1998-11-22

<150> PCT/US97/08793

<151> 1997-05-22

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Trp	Ser	Arg	Asn	Trp	Glu	Asp	Met	Leu	Leu	Gln	Ile	Lys	Ser	Leu	Gly	
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Ile Glu Pro Leu Trp Tyr Thr Asp Ser Phe Ser Glu Gln Asp Tyr Ile	
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Asn Thr Trp Val Glu Val Ala Gln Arg Phe Gly Lys Tyr Trp Asn Val	
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 65 70 75 80
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 115 120 125
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 130 135 140
 Ile Gly Ala Asp Leu Lys Asn Glu Pro His Ser Ser Ser Pro Ala Pro
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 Ala Thr Asp Trp Asn Leu Ala Ala Glu Arg Ile Gly Arg Ala Ile Leu
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 195 200 205
 Thr Pro Glu Ile Asp Gly Arg Tyr Lys Trp Gly His Asn Ala Trp Trp
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 225 230 235 240
 Asp Lys Val Val Tyr Ser Pro Gln Val Tyr Gly Ser Glu Val Tyr Asp
 245 250 255
 Gln Pro Tyr Phe Asp Pro Gly Glu Gly Phe Pro Asp Asn Leu Pro Glu
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 Ile Trp Tyr His His Phe Gly Tyr Val Lys Leu Asp Leu Gly Tyr Pro
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785					790					795					800	
Gly	Asn	Pro	Glu	Phe	Tyr	Ile	Glu	Ile	Asn	Pro	Trp	Asn	Ile	Leu	Ser	
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Ala	Glu	Ser	Tyr	Ala	Glu	Met	Thr	Tyr	Asn	Leu	Ser	Ser	Gly	Val	Leu	
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Ile Ala Ser Lys Asp Glu Gly Val Arg Ser Ala Leu His Phe Ser Met	
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435 440 445	
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Val Met Gly Glu Gly Asn Asp Ser Lys Ile Ile Pro Ala Ile Glu Gly			
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ctt gtg ttt cct tac ttt acg aac tgc cat gag gcg tta aga gaa gac			1776
Leu Val Phe Pro Tyr Phe Thr Asn Cys His Glu Ala Leu Arg Glu Asp			
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gga cgt ttt gga gac tat att cgt gca ctg cga caa cat ttg caa tat			1824
Gly Arg Phe Gly Asp Tyr Ile Arg Ala Leu Arg Gln His Leu Gln Tyr			
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gtg ttg cgg gaa gga att tac cta ttc ccg gac ggg gga tgg aaa att			1872
Val Leu Arg Glu Gly Ile Tyr Leu Phe Pro Asp Gly Gly Trp Lys Ile			
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Cys Leu Asp Lys Gln Gln Leu Val Val Glu Gln Asn Leu Leu Met Pro			
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Ser	Pro	His	Glu	Pro	Gly	Leu	Tyr	His	Ile	Leu	Pro	Phe	Ala	Glu	Thr
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Glu	Arg	Glu	Phe	Arg	Val	Ala	Thr	Asp	Thr	Trp	Lys	Ala	Gly	Asp	Leu
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Thr	Leu	Thr	Ile	Tyr	Ser	Pro	Val	Lys	Ala	Val	Pro	Asp	Pro	Glu	Thr
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Glu	Met	Thr	Ile	Asp	Asn	Thr	Asn	Gly	Thr	Arg	Thr	Arg	Arg	Ala	Phe
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Phe	Gly	Phe	Glu	Gly	Thr	Asp	Pro	Tyr	Thr	Ser	Met	Arg	Gly	Ile	Asp
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Asp	Thr	Cys	Pro	Gln	Leu	Arg	Gly	Val	Gly	Gln	Gly	Arg	Ile	Leu	Gly
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Ile	Ala	Ser	Lys	Asp	Glu	Gly	Val	Arg	Ser	Ala	Leu	His	Phe	Ser	Met
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Thr	Tyr	Gln	Phe	Ala	Val	Cys	Phe	Tyr	Arg	Gly	Gly	Cys	Val	Thr	Ala
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Gly	Met	Asp	Ala	Ser	Tyr	Phe	Tyr	Thr	Arg	Phe	Phe	His	Asn	Ile	Glu
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Glu	Val	Gly	Leu	Tyr	Ala	Leu	Glu	Gln	Ala	Glu	Val	Leu	Lys	Glu	Gln
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Gln	Lys	Phe	Met	Met	Ala	His	Ala	Ile	Arg	Ser	Tyr	Tyr	Gly	Asn	Thr
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Gln	Leu	Leu	Glu	His	Glu	Gly	Lys	Pro	Ile	Trp	Val	Val	Asn	Glu	Gly
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Phe	Glu	Leu	Lys	Met	Asn	Pro	Trp	Thr	Val	Lys	Asn	Val	Leu	Asp	Phe
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Tyr	Val	Glu	Arg	Tyr	Ser	Tyr	Glu	Asp	Arg	Val	Arg	Phe	Pro	Gly	Asp
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Glu	Thr	Glu	Tyr	Pro	Gly	Gly	Ile	Ser	Phe	Thr	His	Asp	Met	Gly	Val
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Ala	Asn	Thr	Phe	Ser	Arg	Pro	His	Tyr	Ser	Ser	Tyr	Glu	Leu	Tyr	Gly
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Ile	Ser	Gly	Cys	Phe	Ser	His	Met	Thr	His	Glu	Gln	Leu	Val	Asn	Trp
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Val	Leu	Cys	Ala	Ala	Val	Tyr	Ile	Glu	Gln	Thr	Lys	Asp	Trp	Ala	Trp
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Arg	Asp	Arg	Arg	Leu	Thr	Ile	Leu	Glu	Gln	Cys	Leu	Glu	Ser	Met	Val
	450				455						460				
Arg	Arg	Asp	His	Pro	Asp	Pro	Glu	Lys	Arg	Asn	Gly	Val	Met	Gly	Leu
465					470					475					480
Asp	Ser	Thr	Arg	Thr	Met	Gly	Gly	Ala	Glu	Ile	Thr	Thr	Tyr	Asp	Ser
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Lys Cys Trp Ala Ala Tyr Val Ala Leu Glu Lys Leu Phe Arg Asp Val
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Gly Lys Glu Glu Leu Ala Ala Leu Ala Arg Glu Gln Ala Glu Lys Cys
      530                      535                      540
Ala Ala Thr Ile Val Ser His Val Thr Glu Asp Gly Tyr Ile Pro Ala
545                      550                      555                      560
Val Met Gly Glu Gly Asn Asp Ser Lys Ile Ile Pro Ala Ile Glu Gly
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Leu Val Phe Pro Tyr Phe Thr Asn Cys His Glu Ala Leu Arg Glu Asp
      580                      585                      590
Gly Arg Phe Gly Asp Tyr Ile Arg Ala Leu Arg Gln His Leu Gln Tyr
      595                      600                      605
Val Leu Arg Glu Gly Ile Tyr Leu Phe Pro Asp Gly Gly Trp Lys Ile
      610                      615                      620
Cys Leu Asp Lys Gln Gln Leu Val Val Glu Gln Asn Leu Leu Met Pro
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Val Tyr Cys Pro Pro His Phe Arg Val Gly Met Gly
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gct gca tcc ggt tcc cat ggg cag acg ttc gcg tac ggc gaa gct ctg          96
Ala Ala Ser Gly Ser His Gly Gln Thr Phe Ala Tyr Gly Glu Ala Leu
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caa aaa tcc atc tat ttt tat gag gct caa cag gcc ggc cca ctc ccg          144
Gln Lys Ser Ile Tyr Phe Tyr Glu Ala Gln Gln Ala Gly Pro Leu Pro
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gaa tgg aac cgc gtt gcc tgg cgt ggc gac tca gtt cct gat gac ggt          192
Glu Trp Asn Arg Val Ala Trp Arg Gly Asp Ser Val Pro Asp Asp Gly
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gcc gac gtc gga ctg gat tta cgc ggt ggc tgg ttc gat gcg ggc gac          240
Ala Asp Val Gly Leu Asp Leu Arg Gly Gly Trp Phe Asp Ala Gly Asp
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cac gtt aag ttt ggc ttt cca atg gcc gcg tca gcg aca ctc gtc gcc          288
His Val Lys Phe Gly Phe Pro Met Ala Ala Ser Ala Thr Leu Val Ala
      85                      90                      95

tgg gga ggc gtc gat tac aaa gac gcg tac gaa cag tcg ggg caa atg          336
Trp Gly Gly Val Asp Tyr Lys Asp Ala Tyr Glu Gln Ser Gly Gln Met
      100                      105                      110

gaa cat ctg cgc aac aac ctg cgc ttc gtc aat gac tac ttt atc agc          384

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Ala His Pro Ala Pro Asn Val Leu Tyr Gly Gln Val Gly Asp Gly Ser	
130 135 140	
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Ala Asp His Thr Phe Trp Gly Pro Ala Glu Val Leu His His Lys Ile	
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ccc ggc tcg cgc att tct atg aag att gac gaa agc tgc ccg ggt acc	528
Pro Gly Ser Arg Ile Ser Met Lys Ile Asp Glu Ser Cys Pro Gly Thr	
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Asp Leu Ala Ala Glu Thr Ala Ala Met Ala Ala Ser Ala Met Val	
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Phe Gln Gly Glu Asp Asp Ala Tyr Ala Ala Thr Leu Ile Thr His Ala	
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Lys Gln Leu Trp Gln Phe Ala Asp Ser Thr Lys Gly Thr Thr Gly Thr	
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Tyr Tyr Gly Leu Met Gly Phe Glu Asn Gln Thr Thr Thr Pro Val Tyr	
275 280 285	
acc tgg tcg ctt ggc tgg aac gat aaa gcg tat gcc gtt tat gta ctt	912
Thr Trp Ser Leu Gly Trp Asn Asp Lys Ala Tyr Ala Val Tyr Val Leu	
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Met Ala Ala Leu Val Gly Asp Glu Val Tyr His Ala Asp Ala Gln Arg	
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tac ctg gat cac tgg agc gtc ggc gag ggt aac cgc aca ccc aat ggg	1008
Tyr Leu Asp His Trp Ser Val Gly Glu Gly Asn Arg Thr Pro Asn Gly	
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Leu Ile Leu Val Asp Ser Trp Gly Val Asn Arg Tyr Ala Ala Asn Ala	
340 345 350	
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Gly Tyr Leu Ala Leu Phe Tyr Ala Asp Ala Ile Gly Ser Asp His Pro	

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aag atc aat tcc tct ggc aac cgc ttc gtg gaa atg aaa gcc gtt att Lys Ile Asn Ser Ser Gly Asn Arg Phe Val Glu Met Lys Ala Val Ile 500 505 510			1536
caa aac cac agc aca aca ccc gcc caa ggt aaa gac gac ctt tac atg Gln Asn His Ser Thr Thr Pro Ala Gln Gly Lys Asp Asp Leu Tyr Met 515 520 525			1584
cgc tat ttc tat gat ctg agc gaa gta ttt gcc gca ggc tac agt ttg Arg Tyr Phe Tyr Asp Leu Ser Glu Val Phe Ala Ala Gly Tyr Ser Leu 530 535 540			1632
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gta caa ttt cgc gtg tcc ctg cca acc aca tcc aat ctt gcc gag tgg Val Gln Phe Arg Val Ser Leu Pro Thr Thr Ser Asn Leu Ala Glu Trp 595 600 605			1824

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 Glu Trp Asn Arg Val Ala Trp Arg Gly Asp Ser Val Pro Asp Asp Gly
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 Ala Asp Val Gly Leu Asp Leu Arg Gly Gly Trp Phe Asp Ala Gly Asp
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 His Val Lys Phe Gly Phe Pro Met Ala Ala Ser Ala Thr Leu Val Ala
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 Trp Gly Gly Val Asp Tyr Lys Asp Ala Tyr Glu Gln Ser Gly Gln Met
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 Glu His Leu Arg Asn Asn Leu Arg Phe Val Asn Asp Tyr Phe Ile Ser
 115 120 125
 Ala His Pro Ala Pro Asn Val Leu Tyr Gly Gln Val Gly Asp Gly Ser
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 Ala Asp His Thr Phe Trp Gly Pro Ala Glu Val Leu His His Lys Ile
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 Pro Gly Ser Arg Ile Ser Met Lys Ile Asp Glu Ser Cys Pro Gly Thr
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 Asp Leu Ala Ala Glu Thr Ala Ala Ala Met Ala Ala Ser Ala Met Val
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 Phe Gln Gly Glu Asp Asp Ala Tyr Ala Ala Thr Leu Ile Thr His Ala
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 Asp Thr Ala Tyr Ser Asn Cys Ile Thr Gly Ala Gln Gly Phe Tyr Thr
 225 230 235 240
 Ser Thr Tyr Gly Val Tyr Tyr Asp Glu Leu Ala Trp Gly Ala Leu Trp
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 Tyr Tyr Gly Leu Met Gly Phe Glu Asn Gln Thr Thr Thr Pro Val Tyr
 275 280 285
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 Tyr Leu Asp His Trp Ser Val Gly Glu Gly Asn Arg Thr Pro Asn Gly
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 Gly Tyr Leu Ala Leu Phe Tyr Ala Asp Ala Ile Gly Ser Asp His Pro
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 485 490 495
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 Gln Ala Asp Gln Leu Val Asn Trp Ala Lys Ala Asn Gly Ile Gly Val
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 His Gly His Thr Leu Val Trp His Ser Glu Tyr Gln Val Pro Asn Trp
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 Met Lys Asn Tyr Ser Gly Asp Ala Thr Ala Phe Gln Thr Met Leu Asn
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acc cat gtg aaa act gtg gct gag cat ttt gct ggc gaa ctg gac agc 240
 Thr His Val Lys Thr Val Ala Glu His Phe Ala Gly Glu Leu Asp Ser
 65 70 75 80

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 Trp Asp Val Val Asn Glu Val Leu Glu Pro Gly Ser Asn Gly Cys Trp
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cgt gaa aac tct ctg ttc tac cag aag ctt ggc aaa gac ttt gtc gcg 336
 Arg Glu Asn Ser Leu Phe Tyr Gln Lys Leu Gly Lys Asp Phe Val Ala
 100 105 110

aac gca ttc cgt gca gct cgc gag ggc gat ccc aat gca gac ttg tat 384
 Asn Ala Phe Arg Ala Ala Arg Glu Gly Asp Pro Asn Ala Asp Leu Tyr
 115 120 125

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 Tyr Asn Asp Tyr Ser Thr Glu Asn Gly Val Thr Ser Asp Glu Lys Phe
 130 135 140

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 Ser Cys Leu Leu Glu Leu Val Asp Glu Leu Leu Glu Ala Asp Val Pro
 145 150 155 160

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 Ile Thr Gly Val Gly Phe Gln Met His Val Gln Ala Thr Trp Pro Ser
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aat gcc aac atc ggc aag gca ttc aaa gcc atc gcg gat cgc ggt ctg 576
 Asn Ala Asn Ile Gly Lys Ala Phe Lys Ala Ile Ala Asp Arg Gly Leu

180	185	190	
aaa gtt aaa att tct gag ctc gat gtt cct gtt aac aac cct tac gga			624
Lys Val Lys Ile Ser Glu Leu Asp Val Pro Val Asn Asn Pro Tyr Gly			
195	200	205	
acc act aat ttc ccg caa tac agc agt ttt acc gcg gaa gcc gcc gag			672
Thr Thr Asn Phe Pro Gln Tyr Ser Ser Phe Thr Ala Glu Ala Ala Glu			
210	215	220	
ctg cag aag cag cgc tac aag ggc att atg caa gcg tac ctt gat aac			720
Leu Gln Lys Gln Arg Tyr Lys Gly Ile Met Gln Ala Tyr Leu Asp Asn			
225	230	235 240	
gta ccg gcc aac ctg cgt ggt ggt ttc acc gtg tgg ggc gtt tgg gat			768
Val Pro Ala Asn Leu Arg Gly Gly Phe Thr Val Trp Gly Val Trp Asp			
245	250	255	
ggc gat agc tgg atc atg acg ttc agc cag tac acc aac gct aac gcc			816
Gly Asp Ser Trp Ile Met Thr Phe Ser Gln Tyr Thr Asn Ala Asn Ala			
260	265	270	
aac gac tgg cca ctg ttg ttc acc ggg ccg taa			849
Asn Asp Trp Pro Leu Leu Phe Thr Gly Pro *			
275	280		

<210> 8
 <211> 282
 <212> PRT
 <213> Bankia gouldi

<400> 8

Met Lys Met Thr Tyr Met His Pro Ala Glu Asp Thr Tyr Ser Phe Gly	
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His Gly His Thr Leu Val Trp His Ser Glu Tyr Gln Val Pro Asn Trp	
35 40 45	
Met Lys Asn Tyr Ser Gly Asp Ala Thr Ala Phe Gln Thr Met Leu Asn	
50 55 60	
Thr His Val Lys Thr Val Ala Glu His Phe Ala Gly Glu Leu Asp Ser	
65 70 75 80	
Trp Asp Val Val Asn Glu Val Leu Glu Pro Gly Ser Asn Gly Cys Trp	
85 90 95	
Arg Glu Asn Ser Leu Phe Tyr Gln Lys Leu Gly Lys Asp Phe Val Ala	
100 105 110	
Asn Ala Phe Arg Ala Ala Arg Glu Gly Asp Pro Asn Ala Asp Leu Tyr	
115 120 125	
Tyr Asn Asp Tyr Ser Thr Glu Asn Gly Val Thr Ser Asp Glu Lys Phe	
130 135 140	
Ser Cys Leu Leu Glu Leu Val Asp Glu Leu Leu Glu Ala Asp Val Pro	
145 150 155 160	
Ile Thr Gly Val Gly Phe Gln Met His Val Gln Ala Thr Trp Pro Ser	
165 170 175	
Asn Ala Asn Ile Gly Lys Ala Phe Lys Ala Ile Ala Asp Arg Gly Leu	
180 185 190	
Lys Val Lys Ile Ser Glu Leu Asp Val Pro Val Asn Asn Pro Tyr Gly	
195 200 205	
Thr Thr Asn Phe Pro Gln Tyr Ser Ser Phe Thr Ala Glu Ala Ala Glu	
210 215 220	

Leu Gln Lys Gln Arg Tyr Lys Gly Ile Met Gln Ala Tyr Leu Asp Asn
 225 230 235 240
 Val Pro Ala Asn Leu Arg Gly Gly Phe Thr Val Trp Gly Val Trp Asp
 245 250 255
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 260 265 270
 Asn Asp Trp Pro Leu Leu Phe Thr Gly Pro
 275 280

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 <211> 3033
 <212> DNA
 <213> Teredinibacter

<220>
 <221> CDS
 <222> (1)...(3033)
 <223> clone # 42GP1

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 1 5 10 15
 gct gtt gcc gcc gca gtt ttc acc acc tct gca gct ttc gcg gat gta 96
 Ala Val Ala Ala Val Phe Thr Thr Ser Ala Ala Phe Ala Asp Val
 20 25 30
 cct ccg ttg aca gtg agc gga aat cag gtt tta agt ggc ggt gaa gca 144
 Pro Pro Leu Thr Val Ser Gly Asn Gln Val Leu Ser Gly Gly Glu Ala
 35 40 45

 aaa agc ttc gct ggt aac agc ttc ttt tgg agc aat acc gga tgg ggc --- 192 ---
 Lys Ser Phe Ala Gly Asn Ser Phe Phe Trp Ser Asn Thr Gly Trp Gly
 50 55 60
 cag gaa cgt ttt tac aac gca gaa act gtg cgt tgg ttg aaa gac gac 240
 Gln Glu Arg Phe Tyr Asn Ala Glu Thr Val Arg Trp Leu Lys Asp Asp
 65 70 75 80
 tgg aac gca acc att gtc cgc gcc gct atg ggc gta gac ttt gat ggc 288
 Trp Asn Ala Thr Ile Val Arg Ala Ala Met Gly Val Asp Phe Asp Gly
 85 90 95
 agc tat atc ccc gag cat gaa gac gcc gac ccc gag ggt aac gtc gct 336
 Ser Tyr Ile Pro Glu His Glu Asp Ala Asp Pro Glu Gly Asn Val Ala
 100 105 110
 cgc gta cgt gca ttg gtg gat gca gcc atc gca gaa gac atg tac gtg 384
 Arg Val Arg Ala Leu Val Asp Ala Ala Ile Ala Glu Asp Met Tyr Val
 115 120 125
 att atc gat ttt cac act cac cac gca gaa gat tac caa gcc gaa tct 432
 Ile Ile Asp Phe His Thr His His Ala Glu Asp Tyr Gln Ala Glu Ser
 130 135 140
 atc gag ttc ttc gaa gaa atg gcc aca ctg tac ggt ggg tac gac aat 480
 Ile Glu Phe Phe Glu Glu Met Ala Thr Leu Tyr Gly Gly Tyr Asp Asn
 145 150 155 160
 gtt att tat gaa atc tat aac gag ccc ctg caa atc agc tgg gac aat 528

Val Ile Tyr Glu Ile Tyr Asn Glu Pro Leu Gln Ile Ser Trp Asp Asn	
165 170 175	
gtt att aaa cct tat gca gaa tcg gtg att ggc gct atc cgc gca atc	576
Val Ile Lys Pro Tyr Ala Glu Ser Val Ile Gly Ala Ile Arg Ala Ile	
180 185 190	
gac ccg gac aac ctg att atc gtc ggc acg ccc act tgg tca cag gac	624
Asp Pro Asp Asn Leu Ile Ile Val Gly Thr Pro Thr Trp Ser Gln Asp	
195 200 205	
gtg gac gcc gct gcg cgc aat cca atc acc agc tac agc aat att gcg	672
Val Asp Ala Ala Ala Arg Asn Pro Ile Thr Ser Tyr Ser Asn Ile Ala	
210 215 220	
tac acc ctg cac ttt tac gca ggc act cac ggt tca tgg ttg cgc gat	720
Tyr Thr Leu His Phe Tyr Ala Gly Thr His Gly Ser Trp Leu Arg Asp	
225 230 235 240	
aaa gcg cgt aac gct atg aac agt ggt att gcg ctg ttt gtg act gag	768
Lys Ala Arg Asn Ala Met Asn Ser Gly Ile Ala Leu Phe Val Thr Glu	
245 250 255	
tgg ggc acc gtt aat gca gat ggc gat ggt gcg cct gca gtt aac gaa	816
Trp Gly Thr Val Asn Ala Asp Gly Asp Gly Ala Pro Ala Val Asn Glu	
260 265 270	
act cag caa tgg atg gac ttc ctc aag cag aac aat atc tct cac ttg	864
Thr Gln Gln Trp Met Asp Phe Leu Lys Gln Asn Asn Ile Ser His Leu	
275 280 285	
aac tgg tcc gtg agt gat aaa ttg gaa ggt gcg tct atc gta caa cct	912
Asn Trp Ser Val Ser Asp Lys Leu Glu Gly Ala Ser Ile Val Gln Pro	
290 295 300	
ggc acg ccc att agc ggc tgg aac gct tct gac ctt acg gcc tcc ggc	960
Gly Thr Pro Ile Ser Gly Trp Asn Ala Ser Asp Leu Thr Ala Ser Gly	
305 310 315 320	
aca ctg gtt aag aac atc gtt tcc aac tgg ggc acc aca atc ggt aac	1008
Thr Leu Val Lys Asn Ile Val Ser Asn Trp Gly Thr Thr Ile Gly Asn	
325 330 335	
ggc agc tcc tca agt tca tcc agc tcc tct tcc agc tct tca agc agt	1056
Gly Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser	
340 345 350	
tct tct tcg agc agt tcc tcc tcc agc agc tct tcc tcg tca agc agc	1104
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser	
355 360 365	
tcc gga tca act ggt ggc ggc aac tgt gct gga gtg aat gtg tac ccg	1152
Ser Gly Ser Thr Gly Gly Gly Asn Cys Ala Gly Val Asn Val Tyr Pro	
370 375 380	
aac tgg acc gcg cgt gac tgg tct ggc ggc gcc tac aac cat gcg aac	1200
Asn Trp Thr Ala Arg Asp Trp Ser Gly Gly Ala Tyr Asn His Ala Asn	
385 390 395 400	
gct ggc gac caa atg gtc tat caa aac agc ctg tat cgt gcc aac tgg	1248
Ala Gly Asp Gln Met Val Tyr Gln Asn Ser Leu Tyr Arg Ala Asn Trp	

405	410	415	
tac acc aac agc gtg cct ggc agc gac gcc tcc tgg act agc ctt ggc Tyr Thr Asn Ser Val Pro Gly Ser Asp Ala Ser Trp Thr Ser Leu Gly 420 425 430			1296
gcc tgc gga ggc aac gga agt acg acc tca tcc agc tca agc agc tcc Ala Cys Gly Gly Asn Gly Ser Thr Ser Ser Ser Ser Ser Ser Ser 435 440 445			1344
tcg tca agc agc agc tct tct tcc agc agc tcc tcg tct act ggc ggt Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Gly Gly 450 455 460			1392
ggc tcc agc tcc tcc agc agt tca tct tct tca tcg tcg tct tcc agc Gly Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser 465 470 475 480			1440
agc tct agc agc act ggt ggc ggt caa tgt acc gaa gtg tgc aac tgg Ser Ser Ser Ser Thr Gly Gly Gly Gln Cys Thr Glu Val Cys Asn Trp 485 490 495			1488
tac ggt cag gga acc tac cca ctg tgt aac aac acc agt ggt tgg ggt Tyr Gly Gln Gly Thr Tyr Pro Leu Cys Asn Asn Thr Ser Gly Trp Gly 500 505 510			1536
tgg gaa aac aat cag agc tgt atc ggc cgt caa acc tgt gag tca cag Trp Glu Asn Asn Gln Ser Cys Ile Gly Arg Gln Thr Cys Glu Ser Gln 515 520 525			1584
aac ggt ggc gct ggc ggc gtg gtg agc aac tgc acc ggt tcg agt aca Asn Gly Gly Ala Gly Gly Val Val Ser Asn Cys Thr Gly Ser Ser Thr 530 535 540			1632
tcc agc agc tcc tct tcc agc agt agt tct tcc tca agt agc agc tcc Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser 545 550 555 560			1680
agt tca tcc agc agc tct tca tct ggc act ggt agc agt aca tct tcc Ser Ser Ser Ser Ser Ser Ser Ser Gly Thr Gly Ser Ser Thr Ser Ser 565 570 575			1728
agc agc agc tct tcc agc agc tcc agc tca agt acc ggt tcc tcc ggt Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Gly Ser Ser Gly 580 585 590			1776
atg cct gga cca cgc gtg gac aac ccc ttc gcc gct gcg cag aag tgg Met Pro Gly Pro Arg Val Asp Asn Pro Phe Ala Ala Ala Gln Lys Trp 595 600 605			1824
tac ata aac cca atg tgg tca gcg agt gct gca aac gaa ccc ggc ggc Tyr Ile Asn Pro Met Trp Ser Ala Ser Ala Ala Asn Glu Pro Gly Gly 610 615 620			1872
tct gtc att gcc aac gaa ccc tcg ttt gta tgg atg gac cgt atc ggc Ser Val Ile Ala Asn Glu Pro Ser Phe Val Trp Met Asp Arg Ile Gly 625 630 635 640			1920
gca atc gaa ggg cct gct gac ggt atg ggc ctg cgc gac cac ttg aac Ala Ile Glu Gly Pro Ala Asp Gly Met Gly Leu Arg Asp His Leu Asn 645 650 655			1968

gaa gcc ctt gca caa ggc gcc gac ctg ttc atg ttt gtt gtg tac gac Glu Ala Leu Ala Gln Gly Ala Asp Leu Phe Met Phe Val Val Tyr Asp 660 665 670	2016
ctg cca aac cgt gac tgt gct gca ctc gcc tcc aac ggt gaa ctg cgc Leu Pro Asn Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Arg 675 680 685	2064
atc tcc gaa gat ggc ttc aac atc tac aag tcc gac tac atc gca cct Ile Ser Glu Asp Gly Phe Asn Ile Tyr Lys Ser Asp Tyr Ile Ala Pro 690 695 700	2112
atc gtt gaa atc atc agc gac cct gca tac gca ggt atc aaa atc gct Ile Val Glu Ile Ile Ser Asp Pro Ala Tyr Ala Gly Ile Lys Ile Ala 705 710 715 720	2160
gcg gtt atc gag gtg gac tca ctg cct aac ctg gtt acc aat ctg agc Ala Val Ile Glu Val Asp Ser Leu Pro Asn Leu Val Thr Asn Leu Ser 725 730 735	2208
gaa cct gac tgt cag gaa gca aat ggt cct ggc ggc tac cgc gac ggc Glu Pro Asp Cys Gln Glu Ala Asn Gly Pro Gly Gly Tyr Arg Asp Gly 740 745 750	2256
att cgt cac gct atc act gaa ctg ggc aaa atc ccc aac gta tac tcc Ile Arg His Ala Ile Thr Glu Leu Gly Lys Ile Pro Asn Val Tyr Ser 755 760 765	2304
tac gtg gat att gca cac tca ggc tgg ctg ggc tgg aac gac aac ttc Tyr Val Asp Ile Ala His Ser Gly Trp Leu Gly Trp Asn Asp Asn Phe 770 775 780	2352
gcg caa ggc gtt aac ctg att tat gaa gtg gtt gcc aac ctc ggt tcc Ala Gln Gly Val Asn Leu Ile Tyr Glu Val Val Ala Asn Leu Gly Ser 785 790 795 800	2400
ggc att aac cca atc gcc ggt ttc gtc agt aac tcc gct aac tac acg Gly Ile Asn Pro Ile Ala Gly Phe Val Ser Asn Ser Ala Asn Tyr Thr 805 810 815	2448
cct gtg gaa gaa ccc ttc ttg cca gac gcc aac ctg cag gtc ggt ggt Pro Val Glu Glu Pro Phe Leu Pro Asp Ala Asn Leu Gln Val Gly Gly 820 825 830	2496
cag ccc gtt cgc tct tcc gat ttc tat gag tgg aac agc tac ctg gca Gln Pro Val Arg Ser Ser Asp Phe Tyr Glu Trp Asn Ser Tyr Leu Ala 835 840 845	2544
gag aaa ccc ttc gtg acc gat tgg cgt tct gcc atg atc tcg aaa ggt Glu Lys Pro Phe Val Thr Asp Trp Arg Ser Ala Met Ile Ser Lys Gly 850 855 860	2592
atg cca agc tcc atc ggt atg ctg atc gat acc gca cgt aac ggc tgg Met Pro Ser Ser Ile Gly Met Leu Ile Asp Thr Ala Arg Asn Gly Trp 865 870 875 880	2640
ggt ggc cct gag cgt cca act gcg cag tct acc tcc aac aac ctg aac Gly Gly Pro Glu Arg Pro Thr Ala Gln Ser Thr Ser Asn Asn Leu Asn 885 890 895	2688

acc ttc gtt aac gaa tca cgt atc gac cgt cgt gag cac cgc ggc aac 2736
 Thr Phe Val Asn Glu Ser Arg Ile Asp Arg Arg Glu His Arg Gly Asn
 900 905 910

tgg tgt aac cag cct ggt ggt gtc ggc tac cgt cca acc gct gca cct 2784
 Trp Cys Asn Gln Pro Gly Gly Val Gly Tyr Arg Pro Thr Ala Ala Pro
 915 920 925

tct cca ggt att gat gcc tac gtt tgg gtg aaa cca cag ggt gag tct 2832
 Ser Pro Gly Ile Asp Ala Tyr Val Trp Val Lys Pro Gln Gly Glu Ser
 930 935 940

gac ggt gtt tcc gat cct aac ttc gag atc gat cct aac gac ccg aac 2880
 Asp Gly Val Ser Asp Pro Asn Phe Glu Ile Asp Pro Asn Asp Pro Asn
 945 950 955 960

aaa cag cac gac cca atg tgt gat ccg ttc gcc agc aac tcg tcc aac 2928
 Lys Gln His Asp Pro Met Cys Asp Pro Phe Ala Ser Asn Ser Ser Asn
 965 970 975

agt gca tac ggc acc ggc gct atg cca aat gct ccg cac gct ggt cgc 2976
 Ser Ala Tyr Gly Thr Gly Ala Met Pro Asn Ala Pro His Ala Gly Arg
 980 985 990

tgg ttc cct gaa gcc ttc cag tta ctg ctt gaa aac gct tac cca cca 3024
 Trp Phe Pro Glu Ala Phe Gln Leu Leu Leu Glu Asn Ala Tyr Pro Pro
 995 1000 1005

att aac taa 3033
 Ile Asn *
 1010

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 <212> PRT
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 Pro Pro Leu Thr Val Ser Gly Asn Gln Val Leu Ser Gly Gly Glu Ala
 35 40 45
 Lys Ser Phe Ala Gly Asn Ser Phe Phe Trp Ser Asn Thr Gly Trp Gly
 50 55 60
 Gln Glu Arg Phe Tyr Asn Ala Glu Thr Val Arg Trp Leu Lys Asp Asp
 65 70 75 80
 Trp Asn Ala Thr Ile Val Arg Ala Ala Met Gly Val Asp Phe Asp Gly
 85 90 95
 Ser Tyr Ile Pro Glu His Glu Asp Ala Asp Pro Glu Gly Asn Val Ala
 100 105 110
 Arg Val Arg Ala Leu Val Asp Ala Ala Ile Ala Glu Asp Met Tyr Val
 115 120 125
 Ile Ile Asp Phe His Thr His His Ala Glu Asp Tyr Gln Ala Glu Ser
 130 135 140
 Ile Glu Phe Phe Glu Glu Met Ala Thr Leu Tyr Gly Gly Tyr Asp Asn
 145 150 155 160
 Val Ile Tyr Glu Ile Tyr Asn Glu Pro Leu Gln Ile Ser Trp Asp Asn
 165 170 175

Val Ile Lys Pro Tyr Ala Glu Ser Val Ile Gly Ala Ile Arg Ala Ile
 180 185 190
 Asp Pro Asp Asn Leu Ile Ile Val Gly Thr Pro Thr Trp Ser Gln Asp
 195 200 205
 Val Asp Ala Ala Ala Arg Asn Pro Ile Thr Ser Tyr Ser Asn Ile Ala
 210 215 220
 Tyr Thr Leu His Phe Tyr Ala Gly Thr His Gly Ser Trp Leu Arg Asp
 225 230 235 240
 Lys Ala Arg Asn Ala Met Asn Ser Gly Ile Ala Leu Phe Val Thr Glu
 245 250 255
 Trp Gly Thr Val Asn Ala Asp Gly Asp Gly Ala Pro Ala Val Asn Glu
 260 265 270
 Thr Gln Gln Trp Met Asp Phe Leu Lys Gln Asn Asn Ile Ser His Leu
 275 280 285
 Asn Trp Ser Val Ser Asp Lys Leu Glu Gly Ala Ser Ile Val Gln Pro
 290 295 300
 Gly Thr Pro Ile Ser Gly Trp Asn Ala Ser Asp Leu Thr Ala Ser Gly
 305 310 315 320
 Thr Leu Val Lys Asn Ile Val Ser Asn Trp Gly Thr Thr Ile Gly Asn
 325 330 335
 Gly Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 340 345 350
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 355 360 365
 Ser Gly Ser Thr Gly Gly Gly Asn Cys Ala Gly Val Asn Val Tyr Pro
 370 375 380
 Asn Trp Thr Ala Arg Asp Trp Ser Gly Gly Ala Tyr Asn His Ala Asn
 385 390 395 400
 Ala Gly Asp Gln Met Val Tyr Gln Asn Ser Leu Tyr Arg Ala Asn Trp
 405 410 415
 Tyr Thr Asn Ser Val Pro Gly Ser Asp Ala Ser Trp Thr Ser Leu Gly
 420 425 430
 Ala Cys Gly Gly Asn Gly Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser
 435 440 445
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Gly Gly
 450 455 460
 Gly Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 465 470 475 480
 Ser Ser Ser Ser Thr Gly Gly Gly Gln Cys Thr Glu Val Cys Asn Trp
 485 490 495
 Tyr Gly Gln Gly Thr Tyr Pro Leu Cys Asn Asn Thr Ser Gly Trp Gly
 500 505 510
 Trp Glu Asn Asn Gln Ser Cys Ile Gly Arg Gln Thr Cys Glu Ser Gln
 515 520 525
 Asn Gly Gly Ala Gly Gly Val Ser Asn Cys Thr Gly Ser Ser Thr
 530 535 540
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 545 550 555 560
 Ser Ser Ser Ser Ser Ser Ser Ser Gly Thr Gly Ser Ser Thr Ser Ser
 565 570 575
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Gly Ser Ser Gly
 580 585 590
 Met Pro Gly Pro Arg Val Asp Asn Pro Phe Ala Ala Ala Gln Lys Trp
 595 600 605
 Tyr Ile Asn Pro Met Trp Ser Ala Ser Ala Ala Asn Glu Pro Gly Gly
 610 615 620
 Ser Val Ile Ala Asn Glu Pro Ser Phe Val Trp Met Asp Arg Ile Gly
 625 630 635 640
 Ala Ile Glu Gly Pro Ala Asp Gly Met Gly Leu Arg Asp His Leu Asn
 645 650 655
 Glu Ala Leu Ala Gln Gly Ala Asp Leu Phe Met Phe Val Val Tyr Asp

660	665	670
Leu Pro Asn Arg Asp Cys Ala Ala	Leu Ala Ser Asn Gly Glu Leu Arg	
675	680	685
Ile Ser Glu Asp Gly Phe Asn Ile Tyr Lys Ser Asp Tyr Ile Ala Pro		
690	695	700
Ile Val Glu Ile Ile Ser Asp Pro Ala Tyr Ala Gly Ile Lys Ile Ala		
705	710	715
Ala Val Ile Glu Val Asp Ser Leu Pro Asn Leu Val Thr Asn Leu Ser		
725	730	735
Glu Pro Asp Cys Gln Glu Ala Asn Gly Pro Gly Gly Tyr Arg Asp Gly		
740	745	750
Ile Arg His Ala Ile Thr Glu Leu Gly Lys Ile Pro Asn Val Tyr Ser		
755	760	765
Tyr Val Asp Ile Ala His Ser Gly Trp Leu Gly Trp Asn Asp Asn Phe		
770	775	780
Ala Gln Gly Val Asn Leu Ile Tyr Glu Val Val Ala Asn Leu Gly Ser		
785	790	795
Gly Ile Asn Pro Ile Ala Gly Phe Val Ser Asn Ser Ala Asn Tyr Thr		
805	810	815
Pro Val Glu Glu Pro Phe Leu Pro Asp Ala Asn Leu Gln Val Gly Gly		
820	825	830
Gln Pro Val Arg Ser Ser Asp Phe Tyr Glu Trp Asn Ser Tyr Leu Ala		
835	840	845
Glu Lys Pro Phe Val Thr Asp Trp Arg Ser Ala Met Ile Ser Lys Gly		
850	855	860
Met Pro Ser Ser Ile Gly Met Leu Ile Asp Thr Ala Arg Asn Gly Trp		
865	870	875
Gly Gly Pro Glu Arg Pro Thr Ala Gln Ser Thr Ser Asn Asn Leu Asn		
885	890	895
Thr Phe Val Asn Glu Ser Arg Ile Asp Arg Arg Glu His Arg Gly Asn		
900	905	910
Trp Cys Asn Gln Pro Gly Gly Val Gly Tyr Arg Pro Thr Ala Ala Pro		
915	920	925
Ser Pro Gly Ile Asp Ala Tyr Val Trp Val Lys Pro Gln Gly Glu Ser		
930	935	940
Asp Gly Val Ser Asp Pro Asn Phe Glu Ile Asp Pro Asn Asp Pro Asn		
945	950	955
Lys Gln His Asp Pro Met Cys Asp Pro Phe Ala Ser Asn Ser Ser Asn		
965	970	975
Ser Ala Tyr Gly Thr Gly Ala Met Pro Asn Ala Pro His Ala Gly Arg		
980	985	990
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Ile Asn		
1010		

<210> 11
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 <212> DNA
 <213> *Microscilla furvescens*

<220>
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 <222> (1)...(1683)
 <223> clone # 53GC1

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ggt att gaa aag ctt gat tac atc aaa agc ctt ggg gtg gat gtt atc Val Ile Glu Lys Leu Asp Tyr Ile Lys Ser Leu Gly Val Asp Val Ile 35 40 45	144
tgg cta tgc ccg gtg tac gat tcc ccc aat gat gac aat ggt tac gat Trp Leu Cys Pro Val Tyr Asp Ser Pro Asn Asp Asp Asn Gly Tyr Asp 50 55 60	192
att cgt gac tac tac gat atc atg gct gat ttc ggc acg atg gct gat Ile Arg Asp Tyr Tyr Asp Ile Met Ala Asp Phe Gly Thr Met Ala Asp 65 70 75 80	240
ttt gat cag ctg ctc gag gga ata cat cag cgt ggg atg aaa ctg cta Phe Asp Gln Leu Leu Glu Gly Ile His Gln Arg Gly Met Lys Leu Leu 85 90 95	288
atg gac ctg gtg gta aac cac tgc tct gat gag cac aaa tgg ttt cag Met Asp Leu Val Val Asn His Cys Ser Asp Glu His Lys Trp Phe Gln 100 105 110	336
gag tcc cgc aag agt aaa gac aac cct tac cgg gac tac ttc atc tgg Glu Ser Arg Lys Ser Lys Asp Asn Pro Tyr Arg Asp Tyr Phe Ile Trp 115 120 125	384
aag cct ggc aaa aac gga ggc cca cct aac aac tgg cag tcc ttt ttt Lys Pro Gly Lys Asn Gly Gly Pro Pro Asn Asn Trp Gln Ser Phe Phe 130 135 140	432
agt ggt aat gcc tgg gaa tac gat gag gcc act gac gag tat tac cta Ser Gly Asn Ala Trp Glu Tyr Asp Glu Ala Thr Asp Glu Tyr Tyr Leu 145 150 155 160	480
cat ctt ttc acc aaa aag caa cca gac ctc aat tgg gaa aac ccg aaa His Leu Phe Thr Lys Lys Gln Pro Asp Leu Asn Trp Glu Asn Pro Lys 165 170 175	528
gta cgt gag gag gtg cac aag ctg atg aag tat tgg ctg gac aaa gga Val Arg Glu Glu Val His Lys Leu Met Lys Tyr Trp Leu Asp Lys Gly 180 185 190	576
gta gat ggg ttc ccg atg gat gtg att tcc gtg att tca aaa aga aac Val Asp Gly Phe Arg Met Asp Val Ile Ser Val Ile Ser Lys Arg Asn 195 200 205	624
ttc gaa gat tca cct tac aag gac ttc aac aag acc atc gat aac gtc Phe Glu Asp Ser Pro Tyr Lys Asp Phe Asn Lys Thr Ile Asp Asn Val 210 215 220	672
tac gcc aat ggc ccg cgt gtg cag gag ttt ctc cag gaa atg aac cgt Tyr Ala Asn Gly Pro Arg Val Gln Glu Phe Leu Gln Glu Met Asn Arg 225 230 235 240	720
gaa gta ctg agt aag tac gat gtg atg aca gta ggt gag ggt cca ggt Glu Val Leu Ser Lys Tyr Asp Val Met Thr Val Gly Glu Gly Pro Gly 245 250 255	768
atc aat ctg gaa agc ggc ctg caa tat gta tcc agc tca gcg gag gct	816

Ile Asn Leu Glu Ser Gly Leu Gln Tyr Val Ser Ser Ser Ala Glu Ala	
260 265 270	
ctt aat atg att ttt cat ttt ggg cac atg ttt atg gat cat gga ccc	864
Leu Asn Met Ile Phe His Phe Gly His Met Phe Met Asp His Gly Pro	
275 280 285	
gga ggt aga ttt gat ccc aag ccc atc gat ttt ctg gaa ttc aaa aaa	912
Gly Gly Arg Phe Asp Pro Lys Pro Ile Asp Phe Leu Glu Phe Lys Lys	
290 295 300	
gtc ttc agg ctg tgg gat gag tac ctt aaa gaa gag ggc tgg ggt agc	960
Val Phe Arg Leu Trp Asp Glu Tyr Leu Lys Glu Glu Gly Trp Gly Ser	
305 310 315 320	
gtc ttt cta ggg aat cat gat ttt cag cga atc gtt tct cgc ttt ggg	1008
Val Phe Leu Gly Asn His Asp Phe Gln Arg Ile Val Ser Arg Phe Gly	
325 330 335	
gat gac gga gcg tac tgg aaa gag tcc gcc aaa ctg ctg agc ttg ttg	1056
Asp Asp Gly Ala Tyr Trp Lys Glu Ser Ala Lys Leu Leu Ser Leu Leu	
340 345 350	
cta ttt agc atg cgc ggc acg gtc tac gtt tac cag ggt gat gaa ata	1104
Leu Phe Ser Met Arg Gly Thr Val Tyr Val Tyr Gln Gly Asp Glu Ile	
355 360 365	
ggt atg acc aat gtg gct ttt gac acc ata gaa gaa tat gac gat gtg	1152
Gly Met Thr Asn Val Ala Phe Asp Thr Ile Glu Glu Tyr Asp Asp Val	
370 375 380	
gag atc aaa aat gct tac aag gag tgg aaa gct gaa gga aaa gac ctg	1200
Glu Ile Lys Asn Ala Tyr Lys Glu Trp Lys Ala Glu Gly Lys Asp Leu	
385 390 395 400	
gat cag ttt tta aag aac gtc cat atc aat ggc cgt gac aat gcc cgt	1248
Asp Gln Phe Leu Lys Asn Val His Ile Asn Gly Arg Asp Asn Ala Arg	
405 410 415	
aca ccg ctg caa tgg aat gat gct gag cag gct ggt ttt acc tca ggc	1296
Thr Pro Leu Gln Trp Asn Asp Ala Glu Gln Ala Gly Phe Thr Ser Gly	
420 425 430	
act cca tgg ctc aaa gtc aac cct aac tat acg gca atc aat gtg gct	1344
Thr Pro Trp Leu Lys Val Asn Pro Asn Tyr Thr Ala Ile Asn Val Ala	
435 440 445	
agt cag gaa gga gat gag aac tct att ctg gca ttt tat cgc cgg atg	1392
Ser Gln Glu Gly Asp Glu Asn Ser Ile Leu Ala Phe Tyr Arg Arg Met	
450 455 460	
gtg gcg atg cga aag gag cac ccg aca ctt gtt tat ggt gat ttt gcc	1440
Val Ala Met Arg Lys Glu His Pro Thr Leu Val Tyr Gly Asp Phe Ala	
465 470 475 480	
ccc att cag gaa gat cat ccg agt gta ttt gct ttt tgg aga tgg gat	1488
Pro Ile Gln Glu Asp His Pro Ser Val Phe Ala Phe Trp Arg Trp Asp	
485 490 495	
gaa gag gct gca tat tta gtc tta ctc aat ttt tct gag gag act cag	1536
Glu Glu Ala Ala Tyr Leu Val Leu Leu Asn Phe Ser Glu Glu Thr Gln	

500	505	510	
gaa ttt ggg ctg gac gat cga ttt gat agt agt aag ctt cgc ata gta			1584
Glu Phe Gly Leu Asp Asp Arg Phe Asp Ser Ser Lys Leu Arg Ile Val			
515	520	525	
gag gcc aat gac ttt gac ttt ggt gag cca caa agt gga aaa gtg aaa			1632
Glu Ala Asn Asp Phe Asp Phe Gly Glu Pro Gln Ser Gly Lys Val Lys			
530	535	540	
cta aaa ccg tgg cag gcg gtg ttg gcg cgt gtt cgg cat att gaa ttg			1680
Leu Lys Pro Trp Gln Ala Val Leu Ala Arg Val Arg His Ile Glu Leu			
545	550	555	560
taa			1683
*			

<210> 12

<211> 560

<212> PRT

<213> *Microscilla furvescens*

<400> 12

Met Asn Lys Lys Trp Trp Lys Glu Ala Val Val Tyr Gln Val Tyr Pro			
1	5	10	15
Arg Ser Phe Lys Asp Ser Asn Gly Asp Gly Val Gly Asp Leu Pro Gly			
20	25	30	
Val Ile Glu Lys Leu Asp Tyr Ile Lys Ser Leu Gly Val Asp Val Ile			
35	40	45	
Trp Leu Cys Pro Val Tyr Asp Ser Pro Asn Asp Asp Asn Gly Tyr Asp			
50	55	60	
Ile Arg Asp Tyr Tyr Asp Ile Met Ala Asp Phe Gly Thr Met Ala Asp			
65	70	75	80
Phe Asp Gln Leu Leu Glu Gly Ile His Gln Arg Gly Met Lys Leu Leu			
85	90	95	
Met Asp Leu Val Val Asn His Cys Ser Asp Glu His Lys Trp Phe Gln			
100	105	110	
Glu Ser Arg Lys Ser Lys Asp Asn Pro Tyr Arg Asp Tyr Phe Ile Trp			
115	120	125	
Lys Pro Gly Lys Asn Gly Gly Pro Pro Asn Asn Trp Gln Ser Phe Phe			
130	135	140	
Ser Gly Asn Ala Trp Glu Tyr Asp Glu Ala Thr Asp Glu Tyr Tyr Leu			
145	150	155	160
His Leu Phe Thr Lys Lys Gln Pro Asp Leu Asn Trp Glu Asn Pro Lys			
165	170	175	
Val Arg Glu Glu Val His Lys Leu Met Lys Tyr Trp Leu Asp Lys Gly			
180	185	190	
Val Asp Gly Phe Arg Met Asp Val Ile Ser Val Ile Ser Lys Arg Asn			
195	200	205	
Phe Glu Asp Ser Pro Tyr Lys Asp Phe Asn Lys Thr Ile Asp Asn Val			
210	215	220	
Tyr Ala Asn Gly Pro Arg Val Gln Glu Phe Leu Gln Glu Met Asn Arg			
225	230	235	240
Glu Val Leu Ser Lys Tyr Asp Val Met Thr Val Gly Glu Gly Pro Gly			
245	250	255	
Ile Asn Leu Glu Ser Gly Leu Gln Tyr Val Ser Ser Ser Ala Glu Ala			
260	265	270	
Leu Asn Met Ile Phe His Phe Gly His Met Phe Met Asp His Gly Pro			
275	280	285	

Gly Gly Arg Phe Asp Pro Lys Pro Ile Asp Phe Leu Glu Phe Lys Lys
 290 295 300
 Val Phe Arg Leu Trp Asp Glu Tyr Leu Lys Glu Glu Gly Trp Gly Ser
 305 310 315 320
 Val Phe Leu Gly Asn His Asp Phe Gln Arg Ile Val Ser Arg Phe Gly
 325 330 335
 Asp Asp Gly Ala Tyr Trp Lys Glu Ser Ala Lys Leu Leu Ser Leu Leu
 340 345 350
 Leu Phe Ser Met Arg Gly Thr Val Tyr Val Tyr Gln Gly Asp Glu Ile
 355 360 365
 Gly Met Thr Asn Val Ala Phe Asp Thr Ile Glu Glu Tyr Asp Asp Val
 370 375 380
 Glu Ile Lys Asn Ala Tyr Lys Glu Trp Lys Ala Glu Gly Lys Asp Leu
 385 390 395 400
 Asp Gln Phe Leu Lys Asn Val His Ile Asn Gly Arg Asp Asn Ala Arg
 405 410 415
 Thr Pro Leu Gln Trp Asn Asp Ala Glu Gln Ala Gly Phe Thr Ser Gly
 420 425 430
 Thr Pro Trp Leu Lys Val Asn Pro Asn Tyr Thr Ala Ile Asn Val Ala
 435 440 445
 Ser Gln Glu Gly Asp Glu Asn Ser Ile Leu Ala Phe Tyr Arg Arg Met
 450 455 460
 Val Ala Met Arg Lys Glu His Pro Thr Leu Val Tyr Gly Asp Phe Ala
 465 470 475 480
 Pro Ile Gln Glu Asp His Pro Ser Val Phe Ala Phe Trp Arg Trp Asp
 485 490 495
 Glu Glu Ala Ala Tyr Leu Val Leu Leu Asn Phe Ser Glu Glu Thr Gln
 500 505 510
 Glu Phe Gly Leu Asp Asp Arg Phe Asp Ser Ser Lys Leu Arg Ile Val
 515 520 525
 Glu Ala Asn Asp Phe Asp Phe Gly Glu Pro Gln Ser Gly Lys Val Lys
 530 535 540
 Leu Lys Pro Trp Gln Ala Val Leu Ala Arg Val Arg His Ile Glu Leu
 545 550 555 560

<210> 13

<211> 1857

<212> DNA

<213> Thermotoga neapolitana

<220>

<221> CDS

<222> (1)...(1857)

<223> clone # 56GC2

<400> 13

tct tct gaa cga ttc tcc act gag cag aaa aga cca gat cat act ctt	48
Ser Ser Glu Arg Phe Ser Thr Glu Gln Lys Arg Pro Asp His Thr Leu	
1 5 10 15	
tgt gga cgg aaa aga aca ttc ggc aaa gaa ggt ggt tat acc acc ctt	96
Cys Gly Arg Lys Arg Thr Phe Gly Lys Glu Gly Gly Tyr Thr Thr Leu	
20 25 30	
caa aga gga aac gct ggt ctt caa agt gaa cgg act gaa gag ggg aga	144
Gln Arg Gly Asn Ala Gly Leu Gln Ser Glu Arg Thr Glu Glu Gly Arg	
35 40 45	
gca cct cgt atc cac cag tct gaa cac ggg aaa aac cat cta tgt gag	192
Ala Pro Arg Ile His Gln Ser Glu His Gly Lys Asn His Leu Cys Glu	
50 55 60	

gtg atc tgt gtg gag atc ttc aaa aga ccg ttc aga gaa ggg agc ttc Val Ile Cys Val Glu Ile Phe Lys Arg Pro Phe Arg Glu Gly Ser Phe 65 70 75 80	240
gtt ctg aaa gag aag gac tac acc gtt gag ttc gag gtg gag aag atc Val Leu Lys Glu Lys Asp Tyr Thr Val Glu Phe Glu Val Glu Lys Ile 85 90 95	288
cat ctt gga tgg aag att tca ggg aga gtg aag gga aat ccc gga agg His Leu Gly Trp Lys Ile Ser Gly Arg Val Lys Gly Asn Pro Gly Arg 100 105 110	336
ctt gag atc ttt cgg aca aac gca ccg aag aaa ctc ctc gtg aac aac Leu Glu Ile Phe Arg Thr Asn Ala Pro Lys Lys Leu Leu Val Asn Asn 115 120 125	384
tgg cag tcc tgg gga ccc tgc agg gtg gtg gat ctt cca tcc ttc acc Trp Gln Ser Trp Gly Pro Cys Arg Val Val Asp Leu Pro Ser Phe Thr 130 135 140	432
cca ccc gag ata gat cca aac tgg cag tac acg gcc tct gtg gta ccg Pro Pro Glu Ile Asp Pro Asn Trp Gln Tyr Thr Ala Ser Val Val Pro 145 150 155 160	480
gat gtg atc aaa aac cgt ctt cag agt gac tac ttc gtg gca gag gaa Asp Val Ile Lys Asn Arg Leu Gln Ser Asp Tyr Phe Val Ala Glu Glu 165 170 175	528
ggg aga gta tac ggt ttt ttg agt tgc aag atc gca cat cct ttc ttt Gly Arg Val Tyr Gly Phe Leu Ser Ser Lys Ile Ala His Pro Phe Phe 180 185 190	576
gcg gca gag aat gga gaa ctt gtt gcg tat ctt gag tac ttc gat gtg Ala Ala Glu Asn Gly Glu Leu Val Ala Tyr Leu Glu Tyr Phe Asp Val 195 200 205	624
aat ttc gat gac ttc gtc ccg ata gaa cct ttt gtc gtc ctt gaa aat Asn Phe Asp Asp Phe Val Pro Ile Glu Pro Phe Val Val Leu Glu Asn 210 215 220	672
cca atc acc tct ctc ctt ctg gaa aag tac gct gaa ctc gtc ggg aag Pro Ile Thr Ser Leu Leu Leu Glu Lys Tyr Ala Glu Leu Val Gly Lys 225 230 235 240	720
gaa aac agc gcg agg att cca aaa cgt aca ccg gtt gga tgg tgc agc Glu Asn Ser Ala Arg Ile Pro Lys Arg Thr Pro Val Gly Trp Cys Ser 245 250 255	768
tgg tac cac tat ttc ctc gat ctc acc tgg gag gag act ttg aag aat Trp Tyr His Tyr Phe Leu Asp Leu Thr Trp Glu Glu Thr Leu Lys Asn 260 265 270	816
ctg gaa ctt gca gga gag ttt ccc ttc gag gtc ttt cag ata gac gac Leu Glu Leu Ala Gly Glu Phe Pro Phe Glu Val Phe Gln Ile Asp Asp 275 280 285	864
gcg tat gaa aaa gac atc gga gac tgg ctc gtc acg aag aaa gac ttc Ala Tyr Glu Lys Asp Ile Gly Asp Trp Leu Val Thr Lys Lys Asp Phe 290 295 300	912

cca tct gtg gac gag atg gca agg acg ata cag gag aaa ggc ttt gtt Pro Ser Val Asp Glu Met Ala Arg Thr Ile Gln Glu Lys Gly Phe Val 305 310 315 320	960
cct ggt ata tgg acc gca ccg ttc agt gtt tca gaa aca tcg gat gtg Pro Gly Ile Trp Thr Ala Pro Phe Ser Val Ser Glu Thr Ser Asp Val 325 330 335	1008
ttc aac tcc tat ccg gac tgg gtc gtg aag gaa aac gga atg cca aag Phe Asn Ser Tyr Pro Asp Trp Val Val Lys Glu Asn Gly Met Pro Lys 340 345 350	1056
atg gcg tac agg aac tgg aac aga aag atc tac gct ctt gac ctt tca Met Ala Tyr Arg Asn Trp Asn Arg Lys Ile Tyr Ala Leu Asp Leu Ser 355 360 365	1104
aac aaa gaa gtc ctg gac tgg ctc ttc gac ctc ttc agc tct ctc aag Asn Lys Glu Val Leu Asp Trp Leu Phe Asp Leu Phe Ser Ser Leu Lys 370 375 380	1152
aag atg ggc tac aga tac ttc aag atc gac ttt ctc ttt gca gga gcg Lys Met Gly Tyr Arg Tyr Phe Lys Ile Asp Phe Leu Phe Ala Gly Ala 385 390 395 400	1200
att ccg ggt gag agg aaa gaa aac atc aca ccc gtt cag gcg ttc aga Ile Pro Gly Glu Arg Lys Glu Asn Ile Thr Pro Val Gln Ala Phe Arg 405 410 415	1248
aag ggg atg gag gtg atc aga aag gcg gtt gga gac ttg ttc ata ctc Lys Gly Met Glu Val Ile Arg Lys Ala Val Gly Asp Leu Phe Ile Leu 420 425 430	1296
gga tgt ggc tct ccc ctt ctt cct gcg gtg ggc tac gtt gac ggc atg Gly Cys Gly Ser Pro Leu Leu Pro Ala Val Gly Tyr Val Asp Gly Met 435 440 445	1344
agg ata ggg ccg gac acc aca ccc ttc tgg ggt gat caa ata gaa gac Arg Ile Gly Pro Asp Thr Thr Pro Phe Trp Gly Asp Gln Ile Glu Asp 450 455 460	1392
aac gga gca ccc gct gca aga tgg gct ctg aga aat gcc atc aca cgt Asn Gly Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg 465 470 475 480	1440
tac ttc atg cac gac aga ctc tgg ctg aac gat ccg gac tgc ctc atc Tyr Phe Met His Asp Arg Leu Trp Leu Asn Asp Pro Asp Cys Leu Ile 485 490 495	1488
ctg aga gag gaa aaa aca gaa ctg acc cca aaa gag aga gag ctc tac Leu Arg Glu Glu Lys Thr Glu Leu Thr Pro Lys Glu Arg Glu Leu Tyr 500 505 510	1536
tcg tac acc tgt ggg atc ctc gac aac atg atc ata gaa agt gac gac Ser Tyr Thr Cys Gly Ile Leu Asp Asn Met Ile Ile Glu Ser Asp Asp 515 520 525	1584
ctg tca ctt gtg aaa gag cac gga agg aag gtt ctg aga gag aca ctc Leu Ser Leu Val Lys Glu His Gly Arg Lys Val Leu Arg Glu Thr Leu 530 535 540	1632
gat ctt ctc ggg gga aag ccc cgt gtt ctg aac atc atg aca gag gat	1680

Asp Leu Leu Gly Gly Lys Pro Arg Val Leu Asn Ile Met Thr Glu Asp
 545 550 555 560

ctg aag tac gag atc gtc tgc tct ggc acg atc tct gga aac acc agg 1728
 Leu Lys Tyr Glu Ile Val Ser Ser Gly Thr Ile Ser Gly Asn Thr Arg
 565 570 575

ctc gtt gtc gat ctc aaa aac aga gag tac cat ctg gaa aaa gag gga 1776
 Leu Val Val Asp Leu Lys Asn Arg Glu Tyr His Leu Glu Lys Glu Gly
 580 585 590

aag tcc tct ctg aga aag aag gtt gtc aaa aga gaa gac gga aga aac 1824
 Lys Ser Ser Leu Arg Lys Lys Val Val Lys Arg Glu Asp Gly Arg Asn
 595 600 605

ttc tac ttc tac gaa gag ggt gag aga gaa tga 1857
 Phe Tyr Phe Tyr Glu Glu Gly Glu Arg Glu *
 610 615

<210> 14

<211> 618

<212> PRT

<213> Thermotoga neapolitana

<400> 14

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 20 25 30
 Gln Arg Gly Asn Ala Gly Leu Gln Ser Glu Arg Thr Glu Glu Gly Arg
 35 40 45
 Ala Pro Arg Ile His Gln Ser Glu His Gly Lys Asn His Leu Cys Glu
 50 55 60
 Val Ile Cys Val Glu Ile Phe Lys Arg Pro Phe Arg Glu Gly Ser Phe
 65 70 75 80
 Val Leu Lys Glu Lys Asp Tyr Thr Val Glu Phe Glu Val Glu Lys Ile
 85 90 95
 His Leu Gly Trp Lys Ile Ser Gly Arg Val Lys Gly Asn Pro Gly Arg
 100 105 110
 Leu Glu Ile Phe Arg Thr Asn Ala Pro Lys Lys Leu Leu Val Asn Asn
 115 120 125
 Trp Gln Ser Trp Gly Pro Cys Arg Val Val Asp Leu Pro Ser Phe Thr
 130 135 140
 Pro Pro Glu Ile Asp Pro Asn Trp Gln Tyr Thr Ala Ser Val Val Pro
 145 150 155 160
 Asp Val Ile Lys Asn Arg Leu Gln Ser Asp Tyr Phe Val Ala Glu Glu
 165 170 175
 Gly Arg Val Tyr Gly Phe Leu Ser Ser Lys Ile Ala His Pro Phe Phe
 180 185 190
 Ala Ala Glu Asn Gly Glu Leu Val Ala Tyr Leu Glu Tyr Phe Asp Val
 195 200 205
 Asn Phe Asp Asp Phe Val Pro Ile Glu Pro Phe Val Val Leu Glu Asn
 210 215 220
 Pro Ile Thr Ser Leu Leu Glu Lys Tyr Ala Glu Leu Val Gly Lys
 225 230 235 240
 Glu Asn Ser Ala Arg Ile Pro Lys Arg Thr Pro Val Gly Trp Cys Ser
 245 250 255
 Trp Tyr His Tyr Phe Leu Asp Leu Thr Trp Glu Glu Thr Leu Lys Asn
 260 265 270
 Leu Glu Leu Ala Gly Glu Phe Pro Phe Glu Val Phe Gln Ile Asp Asp

275	280	285
Ala Tyr Glu Lys Asp Ile Gly Asp Trp Leu Val Thr Lys Lys Asp Phe		
290	295	300
Pro Ser Val Asp Glu Met Ala Arg Thr Ile Gln Glu Lys Gly Phe Val		
305	310	315
Pro Gly Ile Trp Thr Ala Pro Phe Ser Val Ser Glu Thr Ser Asp Val		
	325	330
Phe Asn Ser Tyr Pro Asp Trp Val Val Lys Glu Asn Gly Met Pro Lys		
	340	345
Met Ala Tyr Arg Asn Trp Asn Arg Lys Ile Tyr Ala Leu Asp Leu Ser		
	355	360
Asn Lys Glu Val Leu Asp Trp Leu Phe Asp Leu Phe Ser Ser Leu Lys		
	370	375
Lys Met Gly Tyr Arg Tyr Phe Lys Ile Asp Phe Leu Phe Ala Gly Ala		
385	390	395
Ile Pro Gly Glu Arg Lys Glu Asn Ile Thr Pro Val Gln Ala Phe Arg		
	405	410
Lys Gly Met Glu Val Ile Arg Lys Ala Val Gly Asp Leu Phe Ile Leu		
	420	425
Gly Cys Gly Ser Pro Leu Leu Pro Ala Val Gly Tyr Val Asp Gly Met		
	435	440
Arg Ile Gly Pro Asp Thr Thr Pro Phe Trp Gly Asp Gln Ile Glu Asp		
	450	455
Asn Gly Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg		
465	470	475
Tyr Phe Met His Asp Arg Leu Trp Leu Asn Asp Pro Asp Cys Leu Ile		
	485	490
Leu Arg Glu Glu Lys Thr Glu Leu Thr Pro Lys Glu Arg Glu Leu Tyr		
	500	505
Ser Tyr Thr Cys Gly Ile Leu Asp Asn Met Ile Ile Glu Ser Asp Asp		
	515	520
Leu Ser Leu Val Lys Glu His Gly Arg Lys Val Leu Arg Glu Thr Leu		
	530	535

540	545	550	555	560
Asp Leu Leu Gly Gly Lys Pro Arg Val Leu Asn Ile Met Thr Glu Asp				
545	550	555	560	565
Leu Lys Tyr Glu Ile Val Ser Ser Gly Thr Ile Ser Gly Asn Thr Arg				
	565	570	575	580
Leu Val Val Asp Leu Lys Asn Arg Glu Tyr His Leu Glu Lys Glu Gly				
	580	585	590	595
Lys Ser Ser Leu Arg Lys Lys Val Val Lys Arg Glu Asp Gly Arg Asn				
	595	600	605	610
Phe Tyr Phe Tyr Glu Glu Gly Glu Arg Glu				
	610	615		

<210> 15
 <211> 2001
 <212> DNA
 <213> Thermotoga neapolitana

<220>
 <221> CDS
 <222> (1)...(2001)
 <223> clone # 56GP1

<400> 15

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Met	Arg	Lys	Leu	Val	Phe	Ser	Phe	Leu	Ile	Val	Thr	Leu	Pro	Ile	Val
1			5					10					15		

48

ctc	ttt	gca	aac	agt	gat	ttc	gtg	aaa	gtg	gaa	aac	ggc	agg	ttc	ata
Leu	Phe	Ala	Asn	Ser	Asp	Phe	Val	Lys	Val	Glu	Asn	Gly	Arg	Phe	Ile

96

20	25	30	
ctg aac gga gaa gag ttc aga ttc gtt gga agc aac aac tac tac atg Leu Asn Gly Glu Glu Phe Arg Phe Val Gly Ser Asn Asn Tyr Tyr Met 35 40 45			144
cac tac aag agc aat cga atg ata gac agt gtc ctt gaa agt gca aaa His Tyr Lys Ser Asn Arg Met Ile Asp Ser Val Leu Glu Ser Ala Lys 50 55 60			192
gcc atg ggg gtg aag gtg ctc aga att tgg gga ttc ctc gat ggt gag Ala Met Gly Val Lys Val Leu Arg Ile Trp Gly Phe Leu Asp Gly Glu 65 70 75 80			240
agt tac tgc cgt gac aag aac acc tac atg cac ccc gca ccg gga gta Ser Tyr Cys Arg Asp Lys Asn Thr Tyr Met His Pro Ala Pro Gly Val 85 90 95			288
ttt gga ttg cca gag ggt acg aac gct cag gac ggt ttt gaa aga ctc Phe Gly Leu Pro Glu Gly Thr Asn Ala Gln Asp Gly Phe Glu Arg Leu 100 105 110			336
gac tac acg gta gcg aaa gca aaa gaa ctg ggc ata aag ctc ata atc Asp Tyr Thr Val Ala Lys Ala Lys Glu Leu Gly Ile Lys Leu Ile Ile 115 120 125			384
gtt ctt gtg aac aac tgg gac gac ttc ggt gga atg aat caa tac gtg Val Leu Val Asn Asn Trp Asp Asp Phe Gly Gly Met Asn Gln Tyr Val 130 135 140			432
aga tgg ttt ggg ggc atc cat cac gat gac ttc tac agg aac gag aag Arg Trp Phe Gly Gly Ile His His Asp Asp Phe Tyr Arg Asn Glu Lys 145 150 155 160			480
atc aaa gaa gaa tac aaa aag tac gtg tct ttc ctc ata aac agg gtg Ile Lys Glu Glu Tyr Lys Lys Tyr Val Ser Phe Leu Ile Asn Arg Val 165 170 175			528
aac acc tac acg ggt gtt cct tac agg gaa gag ccc acc atc atg gca Asn Thr Tyr Thr Gly Val Pro Tyr Arg Glu Glu Pro Thr Ile Met Ala 180 185 190			576
tgg gaa ctg gcg aac gag ccc agg tgt gaa acg gac aag tct ggt aac Trp Glu Leu Ala Asn Glu Pro Arg Cys Glu Thr Asp Lys Ser Gly Asn 195 200 205			624
aca ctc gtt gaa tgg gta gag gag atg agt gct tac ata aag agt ctg Thr Leu Val Glu Trp Val Glu Glu Met Ser Ala Tyr Ile Lys Ser Leu 210 215 220			672
gat cca aac cac ctg gtt gcc gtg gga gac gag gga ttc ttc aac aac Asp Pro Asn His Leu Val Ala Val Gly Asp Glu Gly Phe Phe Asn Asn 225 230 235 240			720
tac gaa ggc ttc aga cct tac ggt gga gag gct gag tgg gcc tac aac Tyr Glu Gly Phe Arg Pro Tyr Gly Gly Glu Ala Glu Trp Ala Tyr Asn 245 250 255			768
gga tgg tcc ggt gtt gac tgg aag aga ctt ctg gag ata gag acg gtg Gly Trp Ser Gly Val Asp Trp Lys Arg Leu Leu Glu Ile Glu Thr Val 260 265 270			816

gat ttt ggt acg ttc cat ctc tac ccc tcc cac tgg ggt gtg agc cct Asp Phe Gly Thr Phe His Leu Tyr Pro Ser His Trp Gly Val Ser Pro 275 280 285	864
gaa aac tac gca cag tgg ggg gca aag tgg ata gaa gat cac ata aag Glu Asn Tyr Ala Gln Trp Gly Ala Lys Trp Ile Glu Asp His Ile Lys 290 295 300	912
atc gca aaa gag gtt gga aaa ccc gtc gtt ctg gaa gag tac ggt att Ile Ala Lys Glu Val Gly Lys Pro Val Val Leu Glu Glu Tyr Gly Ile 305 310 315 320	960
ccc aaa agt gcc ccg gtc aac agg gtt gcc att tac aaa ttg tgg aac Pro Lys Ser Ala Pro Val Asn Arg Val Ala Ile Tyr Lys Leu Trp Asn 325 330 335	1008
gat ctg gtc tac aac ctc ggt gga aac ggt gcc atg ttc tgg atg ctc Asp Leu Val Tyr Asn Leu Gly Gly Asn Gly Ala Met Phe Trp Met Leu 340 345 350	1056
gca gga atc ggt gaa gga tgg gac aga gac gaa aag ggt tac tac ccc Ala Gly Ile Gly Glu Gly Trp Asp Arg Asp Glu Lys Gly Tyr Tyr Pro 355 360 365	1104
gat tac gac ggc ttc aga ata gtg aac gat gaa agt gaa gag gca aag Asp Tyr Asp Gly Phe Arg Ile Val Asn Asp Glu Ser Glu Glu Ala Lys 370 375 380	1152
ttg atc aga gag tac gcg aaa ctg ttc agc acg ggt gag gat acg agg Leu Ile Arg Glu Tyr Ala Lys Leu Phe Ser Thr Gly Glu Asp Thr Arg 385 390 395 400	1200
gaa gat acc tgc atg ttc atc aca cca aag gat ggt cag gag atc aaa Glu Asp Thr Cys Met Phe Ile Thr Pro Lys Asp Gly Gln Glu Ile Lys 405 410 415	1248
aag act gtg aag gtg aga gtg ggt gtc ttc gac tac agc aac acg ttc Lys Thr Val Lys Val Arg Val Gly Val Phe Asp Tyr Ser Asn Thr Phe 420 425 430	1296
aaa gga att tcc gtc ggg gtt gaa aat ctg ctc ttt gaa gat gag ata Lys Gly Ile Ser Val Gly Val Glu Asn Leu Leu Phe Glu Asp Glu Ile 435 440 445	1344
aaa cat ctc gga tat gga gtt tac gga ttc gaa ttt gac aca acg cgg Lys His Leu Gly Tyr Gly Val Tyr Gly Phe Glu Phe Asp Thr Thr Arg 450 455 460	1392
att tca gac gga gaa cac gag atg ttc ctt gag gca cat ttc agg gga Ile Ser Asp Gly Glu His Glu Met Phe Leu Glu Ala His Phe Arg Gly 465 470 475 480	1440
gaa acg gtg aaa gac aca atc agg gtg aaa gtt gtg aac aga gcg cag Glu Thr Val Lys Asp Thr Ile Arg Val Lys Val Val Asn Arg Ala Gln 485 490 495	1488
tat gta ctc gca gaa gaa gtg gat ttt tcc aga ccc gaa gaa gtc aag Tyr Val Leu Ala Glu Glu Val Asp Phe Ser Arg Pro Glu Glu Val Lys 500 505 510	1536

aac tgg tgg aac agc gga aca tgg cag gct gag ttc aaa aca ccc gat 1584
 Asn Trp Trp Asn Ser Gly Thr Trp Gln Ala Glu Phe Lys Thr Pro Asp
 515 520 525
 ata gag tgg aac ggt gag gtg ggg aac ggt gct ctc cag atg aac gtg 1632
 Ile Glu Trp Asn Gly Glu Val Gly Asn Gly Ala Leu Gln Met Asn Val
 530 535 540
 gtg ctt ccc gga aag ggt gac tgg gaa gag gtg agg gtg gtc agg aaa 1680
 Val Leu Pro Gly Lys Gly Asp Trp Glu Glu Val Arg Val Val Arg Lys
 545 550 555 560
 ttc gat caa ctc ccc gtg tgt gag atc ctc gag tac gat atc tac ata 1728
 Phe Asp Gln Leu Pro Val Cys Glu Ile Leu Glu Tyr Asp Ile Tyr Ile
 565 570 575
 cca gac gtt gaa ggg ctt aca gga agg ctc aga ccg tac gcg gtg ctg 1776
 Pro Asp Val Glu Gly Leu Thr Gly Arg Leu Arg Pro Tyr Ala Val Leu
 580 585 590
 aat ccc ggc tgg gtg aag ata ggg ctc gac atg aac aac acc tcg att 1824
 Asn Pro Gly Trp Val Lys Ile Gly Leu Asp Met Asn Asn Thr Ser Ile
 595 600 605
 gac agc gga gaa ctt gtc agt ttc gat ggc aaa aag tac aga aag ttc 1872
 Asp Ser Gly Glu Leu Val Ser Phe Asp Gly Lys Lys Tyr Arg Lys Phe
 610 615 620
 cat gtg agg atc gag ttc gac aag aca cct gga gtg aac gag ctc cac 1920
 His Val Arg Ile Glu Phe Asp Lys Thr Pro Gly Val Asn Glu Leu His
 625 630 635 640
 ata ggt gta gtt gga gac cac ctg gag tat gat ggg ccg att ttc atc 1968
 Ile Gly Val Val Gly Asp His Leu Glu Tyr Asp Gly Pro Ile Phe Ile
 645 650 655
 gat aat gtg agg ctc tat aaa aaa tct tct tga 2001
 Asp Asn Val Arg Leu Tyr Lys Lys Ser Ser *
 660 665

<210> 16

<211> 666

<212> PRT

<213> Thermotoga neapolitana

<400> 16

Met Arg Lys Leu Val Phe Ser Phe Leu Ile Val Thr Leu Pro Ile Val
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 Leu Phe Ala Asn Ser Asp Phe Val Lys Val Glu Asn Gly Arg Phe Ile
 20 25 30
 Leu Asn Gly Glu Glu Phe Arg Phe Val Gly Ser Asn Asn Tyr Tyr Met
 35 40 45
 His Tyr Lys Ser Asn Arg Met Ile Asp Ser Val Leu Glu Ser Ala Lys
 50 55 60
 Ala Met Gly Val Lys Val Leu Arg Ile Trp Gly Phe Leu Asp Gly Glu
 65 70 75 80
 Ser Tyr Cys Arg Asp Lys Asn Thr Tyr Met His Pro Ala Pro Gly Val
 85 90 95
 Phe Gly Leu Pro Glu Gly Thr Asn Ala Gln Asp Gly Phe Glu Arg Leu
 100 105 110

Asp Tyr Thr Val Ala Lys Ala Lys Glu Leu Gly Ile Lys Leu Ile Ile
 115 120 125
 Val Leu Val Asn Asn Trp Asp Asp Phe Gly Gly Met Asn Gln Tyr Val
 130 135 140
 Arg Trp Phe Gly Gly Ile His His Asp Asp Phe Tyr Arg Asn Glu Lys
 145 150 155 160
 Ile Lys Glu Glu Tyr Lys Lys Tyr Val Ser Phe Leu Ile Asn Arg Val
 165 170 175
 Asn Thr Tyr Thr Gly Val Pro Tyr Arg Glu Glu Pro Thr Ile Met Ala
 180 185 190
 Trp Glu Leu Ala Asn Glu Pro Arg Cys Glu Thr Asp Lys Ser Gly Asn
 195 200 205
 Thr Leu Val Glu Trp Val Glu Glu Met Ser Ala Tyr Ile Lys Ser Leu
 210 215 220
 Asp Pro Asn His Leu Val Ala Val Gly Asp Glu Gly Phe Phe Asn Asn
 225 230 235 240
 Tyr Glu Gly Phe Arg Pro Tyr Gly Gly Glu Ala Glu Trp Ala Tyr Asn
 245 250 255
 Gly Trp Ser Gly Val Asp Trp Lys Arg Leu Leu Glu Ile Glu Thr Val
 260 265 270
 Asp Phe Gly Thr Phe His Leu Tyr Pro Ser His Trp Gly Val Ser Pro
 275 280 285
 Glu Asn Tyr Ala Gln Trp Gly Ala Lys Trp Ile Glu Asp His Ile Lys
 290 295 300
 Ile Ala Lys Glu Val Gly Lys Pro Val Val Leu Glu Glu Tyr Gly Ile
 305 310 315 320
 Pro Lys Ser Ala Pro Val Asn Arg Val Ala Ile Tyr Lys Leu Trp Asn
 325 330 335
 Asp Leu Val Tyr Asn Leu Gly Gly Asn Gly Ala Met Phe Trp Met Leu
 340 345 350
 Ala Gly Ile Gly Glu Gly Trp Asp Arg Asp Glu Lys Gly Tyr Tyr Pro
 355 360 365
 Asp Tyr Asp Gly Phe Arg Ile Val Asn Asp Glu Ser Glu Glu Ala Lys
 370 375 380
 Leu Ile Arg Glu Tyr Ala Lys Leu Phe Ser Thr Gly Glu Asp Thr Arg
 385 390 395 400
 Glu Asp Thr Cys Met Phe Ile Thr Pro Lys Asp Gly Gln Glu Ile Lys
 405 410 415
 Lys Thr Val Lys Val Arg Val Gly Val Phe Asp Tyr Ser Asn Thr Phe
 420 425 430
 Lys Gly Ile Ser Val Gly Val Glu Asn Leu Leu Phe Glu Asp Glu Ile
 435 440 445
 Lys His Leu Gly Tyr Gly Val Tyr Gly Phe Glu Phe Asp Thr Thr Arg
 450 455 460
 Ile Ser Asp Gly Glu His Glu Met Phe Leu Glu Ala His Phe Arg Gly
 465 470 475 480
 Glu Thr Val Lys Asp Thr Ile Arg Val Lys Val Val Asn Arg Ala Gln
 485 490 495
 Tyr Val Leu Ala Glu Glu Val Asp Phe Ser Arg Pro Glu Glu Val Lys
 500 505 510
 Asn Trp Trp Asn Ser Gly Thr Trp Gln Ala Glu Phe Lys Thr Pro Asp
 515 520 525
 Ile Glu Trp Asn Gly Glu Val Gly Asn Gly Ala Leu Gln Met Asn Val
 530 535 540
 Val Leu Pro Gly Lys Gly Asp Trp Glu Glu Val Arg Val Val Arg Lys
 545 550 555 560
 Phe Asp Gln Leu Pro Val Cys Glu Ile Leu Glu Tyr Asp Ile Tyr Ile
 565 570 575
 Pro Asp Val Glu Gly Leu Thr Gly Arg Leu Arg Pro Tyr Ala Val Leu
 580 585 590
 Asn Pro Gly Trp Val Lys Ile Gly Leu Asp Met Asn Asn Thr Ser Ile

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      595              600              605
Asp Ser Gly Glu Leu Val Ser Phe Asp Gly Lys Lys Tyr Arg Lys Phe
  610              615              620
His Val Arg Ile Glu Phe Asp Lys Thr Pro Gly Val Asn Glu Leu His
  625              630              635              640
Ile Gly Val Val Gly Asp His Leu Glu Tyr Asp Gly Pro Ile Phe Ile
      645              650              655
Asp Asn Val Arg Leu Tyr Lys Lys Ser Ser
      660              665

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<210> 17
 <211> 255
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Alum Rock sulfur spring (clone # 58GB3)

<221> CDS
 <222> (1)...(255)

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<400> 17
atg cat ttt agc cca cta caa ttg atc ctc gtc tta gtc att gtc att      48
Met His Phe Ser Pro Leu Gln Leu Ile Leu Val Leu Val Ile Val Ile
  1              5              10              15

ctg ctg ttt ggc acc aaa aaa tta cgc aat atg ggc ggc gat tta ggc      96
Leu Leu Phe Gly Thr Lys Lys Leu Arg Asn Met Gly Gly Asp Leu Gly
      20              25              30

gaa gcc ttc aag aat ttc aga aaa gca gtc aaa gac ggc gat gat gct      144
Glu Ala Phe Lys Asn Phe Arg Lys Ala Val Lys Asp Gly Asp Asp Ala
      35              40              45
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gaa aca caa aaa gat gtt gct gtg caa aaa gtt gac caa cag cca cca      192
Glu Thr Gln Lys Asp Val Ala Val Gln Lys Val Asp Gln Gln Pro Pro
  50              55              60

gca cag ccc atc cca caa ggt cga gtc att gat tcg gaa gcc aag gaa      240
Ala Gln Pro Ile Pro Gln Gly Arg Val Ile Asp Ser Glu Ala Lys Glu
  65              70              75              80

aag gat aag gtc taa
Lys Asp Lys Val *      255

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<210> 18
 <211> 84
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Alum Rock sulfur spring (clone # 58GB3)

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<400> 18
Met His Phe Ser Pro Leu Gln Leu Ile Leu Val Leu Val Ile Val Ile
  1              5              10              15
Leu Leu Phe Gly Thr Lys Lys Leu Arg Asn Met Gly Gly Asp Leu Gly
      20              25              30
Glu Ala Phe Lys Asn Phe Arg Lys Ala Val Lys Asp Gly Asp Asp Ala

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35 40 45
 Glu Thr Gln Lys Asp Val Ala Val Gln Lys Val Asp Gln Gln Pro Pro
 50 55 60
 Ala Gln Pro Ile Pro Gln Gly Arg Val Ile Asp Ser Glu Ala Lys Glu
 65 70 75 80
 Lys Asp Lys Val

<210> 19
 <211> 1479
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> AEPII 1a (clone # 63GA3)

<221> CDS
 <222> (1)...(1479)

<400> 19
 atg gaa gga ctt cga gga ggt gtg agg atg aag ttc cca tct aac ttt 48
 Met Glu Gly Leu Arg Gly Gly Val Arg Met Lys Phe Pro Ser Asn Phe
 1 5 10 15

 ctt ttt ggc tac tcc tgg tgc ggc ttc cag ttt gaa atg ggt tta cct 96
 Leu Phe Gly Tyr Ser Trp Ser Gly Phe Gln Phe Glu Met Gly Leu Pro
 20 25 30

 ggg agt gaa gtt gag agc gac tgg tgg gca tgg gtc cac gat aag gag 144
 Gly Ser Glu Val Glu Ser Asp Trp Trp Ala Trp Val His Asp Lys Glu
 35 40 45

 --- aac atc ttc tgc ggc cta gtt agc ggt gac cta cca gag aac ggg cct --- 192 ---
 Asn Ile Phe Ser Gly Leu Val Ser Gly Asp Leu Pro Glu Asn Gly Pro
 50 55 60

 gct tac tgg cac ctc tac aag aaa gac cac gac ata gct gaa agc ctt 240
 Ala Tyr Trp His Leu Tyr Lys Lys Asp His Asp Ile Ala Glu Ser Leu
 65 70 75 80

 ggc atg gac gcg ata aga ggc gga atc gag tgg gcg agg atc ttc cca 288
 Gly Met Asp Ala Ile Arg Gly Gly Ile Glu Trp Ala Arg Ile Phe Pro
 85 90 95

 aaa ccc acc ttt gac gtg aag gtt gac gtg gaa aag gac gaa aac ggg 336
 Lys Pro Thr Phe Asp Val Lys Val Asp Val Glu Lys Asp Glu Asn Gly
 100 105 110

 aac ata atc tcc att gac gtc ccg gag agc gcg ata gag gag cta gaa 384
 Asn Ile Ile Ser Ile Asp Val Pro Glu Ser Ala Ile Glu Glu Leu Glu
 115 120 125

 aag ctt gcc aac atg gat gcc ctc aac cac tac cgc gaa atc tac tgc 432
 Lys Leu Ala Asn Met Asp Ala Leu Asn His Tyr Arg Glu Ile Tyr Ser
 130 135 140

 gac tgg aag gag agg ggc aag acc ttc ata ttg aac ctc tat cac tgg 480
 Asp Trp Lys Glu Arg Gly Lys Thr Phe Ile Leu Asn Leu Tyr His Trp
 145 150 155 160

 ccc ctt ccc ctc tgg ctc cac gac ccg ata ggc gtt aga aag ctc ggc 528

Pro	Leu	Pro	Leu	Trp	Leu	His	Asp	Pro	Ile	Gly	Val	Arg	Lys	Leu	Gly	
				165					170					175		
cct	gat	aga	gct	ccc	tcg	ggc	tgg	ctg	gac	gag	agg	agc	gtg	gtg	gag	576
Pro	Asp	Arg	Ala	Pro	Ser	Gly	Trp	Leu	Asp	Glu	Arg	Ser	Val	Val	Glu	
			180					185					190			
ttc	acc	aag	ttc	gct	gca	ttc	atc	gcc	tac	cac	ttg	gat	gac	ctc	gtt	624
Phe	Thr	Lys	Phe	Ala	Ala	Phe	Ile	Ala	Tyr	His	Leu	Asp	Asp	Leu	Val	
		195					200					205				
gac	atg	tgg	agc	acg	atg	aac	gag	ccg	aat	gtg	ggt	tac	gag	cag	ggt	672
Asp	Met	Trp	Ser	Thr	Met	Asn	Glu	Pro	Asn	Val	Val	Tyr	Glu	Gln	Gly	
	210					215				220						
tac	acg	agg	cct	cag	tcg	ggc	ttt	cca	ccg	ggt	tat	ctc	agc	cac	gag	720
Tyr	Thr	Arg	Pro	Gln	Ser	Gly	Phe	Pro	Pro	Gly	Tyr	Leu	Ser	His	Glu	
225				230						235					240	
gcc	gct	gga	aag	gcg	aag	ctc	aac	ctc	atg	cag	gct	cac	gct	aga	gct	768
Ala	Ala	Gly	Lys	Ala	Lys	Leu	Asn	Leu	Met	Gln	Ala	His	Ala	Arg	Ala	
				245					250					255		
tac	gat	gcg	ata	aaa	gag	cac	tcg	gac	aag	ccc	gtg	ggg	ttg	ata	tac	816
Tyr	Asp	Ala	Ile	Lys	Glu	His	Ser	Asp	Lys	Pro	Val	Gly	Leu	Ile	Tyr	
			260					265					270			
tcc	ttt	gtc	tgg	cac	gat	gcc	cta	aac	gag	gaa	gcg	gag	gag	att	gtg	864
Ser	Phe	Val	Trp	His	Asp	Ala	Leu	Asn	Glu	Glu	Ala	Glu	Glu	Ile	Val	
		275					280					285				
aag	gag	ata	agg	agg	aga	cac	tac	gac	ttc	gta	acc	ggc	ctt	cac	tcc	912
Lys	Glu	Ile	Arg	Arg	Arg	His	Tyr	Asp	Phe	Val	Thr	Gly	Leu	His	Ser	
	290					295					300					
ggc	tca	tcg	gag	ttc	ggg	gag	agg	gag	gac	ttc	aag	ggg	aag	atc	gac	960
Gly	Ser	Ser	Glu	Phe	Gly	Glu	Arg	Glu	Asp	Phe	Lys	Gly	Lys	Ile	Asp	
305				310						315				320		
tgg	ata	ggc	gtg	aac	tac	tac	act	agg	ggt	gct	tac	gag	atg	agg	aac	1008
Trp	Ile	Gly	Val	Asn	Tyr	Tyr	Thr	Arg	Val	Ala	Tyr	Glu	Met	Arg	Asn	
				325					330					335		
ggc	cgc	ttt	atg	gcc	cta	ccc	ggg	tac	ggc	tac	atg	tgc	gag	agg	agt	1056
Gly	Arg	Phe	Met	Ala	Leu	Pro	Gly	Tyr	Gly	Tyr	Met	Cys	Glu	Arg	Ser	
			340					345					350			
ggt	tac	gca	aaa	tcc	gga	agg	ccc	gcg	agc	gat	ttt	ggc	tgg	gag	acc	1104
Gly	Tyr	Ala	Lys	Ser	Gly	Arg	Pro	Ala	Ser	Asp	Phe	Gly	Trp	Glu	Thr	
		355					360					365				
tat	cct	gag	ggc	ctc	gaa	aac	gtc	ctg	atg	gat	ctg	aag	gag	ctc	tac	1152
Tyr	Pro	Glu	Gly	Leu	Glu	Asn	Val	Leu	Met	Asp	Leu	Lys	Glu	Leu	Tyr	
	370					375					380					
ggc	ctg	cca	atg	atg	gtg	acg	gag	aac	ggg	atg	gcg	gat	atg	gca	gac	1200
Gly	Leu	Pro	Met	Met	Val	Thr	Glu	Asn	Gly	Met	Ala	Asp	Met	Ala	Asp	
385					390				395					400		
agg	cac	cgc	tct	tac	tac	ctc	gtg	agc	cac	ctc	gcg	gct	atc	cac	agg	1248
Arg	His	Arg	Ser	Tyr	Tyr	Leu	Val	Ser	His	Leu	Ala	Ala	Ile	His	Arg	

405	410	415	
gcg atg gag aag ggt gcc gac gtt agg ggg tac ctc cac tgg tct ctg			1296
Ala Met Glu Lys Gly Ala Asp Val Arg Gly Tyr Leu His Trp Ser Leu			
420	425	430	
acc gac aac tac gag tgg gcg cag ggc ttc aga atg cgc ttt ggg ctg			1344
Thr Asp Asn Tyr Glu Trp Ala Gln Gly Phe Arg Met Arg Phe Gly Leu			
435	440	445	
gtg atg gtg gac ttc gag act aag aag cgc tac ata agg ccg agc gca			1392
Val Met Val Asp Phe Glu Thr Lys Lys Arg Tyr Ile Arg Pro Ser Ala			
450	455	460	
ctc gtc ttc agg gag ata gcc acg cag aag gaa ata ccc gaa gag ctc			1440
Leu Val Phe Arg Glu Ile Ala Thr Gln Lys Glu Ile Pro Glu Glu Leu			
465	470	475	480
tcc cac cta gcg aac ctc gaa ctg gta acg aag aag taa			1479
Ser His Leu Ala Asn Leu Glu Leu Val Thr Lys Lys *			
485	490		
<210> 20			
<211> 492			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> AEPII 1a (clone # 63GP4)			
<400> 20			
Met Glu Gly Leu Arg Gly Gly Val Arg Met Lys Phe Pro Ser Asn Phe			
1 5 10 15			
Leu Phe Gly Tyr Ser Trp Ser Gly Phe Gln Phe Glu Met Gly Leu Pro			
20 25 30			
Gly Ser Glu Val Glu Ser Asp Trp Trp Ala Trp Val His Asp Lys Glu			
35 40 45			
Asn Ile Phe Ser Gly Leu Val Ser Gly Asp Leu Pro Glu Asn Gly Pro			
50 55 60			
Ala Tyr Trp His Leu Tyr Lys Lys Asp His Asp Ile Ala Glu Ser Leu			
65 70 75 80			
Gly Met Asp Ala Ile Arg Gly Gly Ile Glu Trp Ala Arg Ile Phe Pro			
85 90 95			
Lys Pro Thr Phe Asp Val Lys Val Asp Val Glu Lys Asp Glu Asn Gly			
100 105 110			
Asn Ile Ile Ser Ile Asp Val Pro Glu Ser Ala Ile Glu Glu Leu Glu			
115 120 125			
Lys Leu Ala Asn Met Asp Ala Leu Asn His Tyr Arg Glu Ile Tyr Ser			
130 135 140			
Asp Trp Lys Glu Arg Gly Lys Thr Phe Ile Leu Asn Leu Tyr His Trp			
145 150 155 160			
Pro Leu Pro Leu Trp Leu His Asp Pro Ile Gly Val Arg Lys Leu Gly			
165 170 175			
Pro Asp Arg Ala Pro Ser Gly Trp Leu Asp Glu Arg Ser Val Val Glu			
180 185 190			
Phe Thr Lys Phe Ala Ala Phe Ile Ala Tyr His Leu Asp Asp Leu Val			
195 200 205			
Asp Met Trp Ser Thr Met Asn Glu Pro Asn Val Val Tyr Glu Gln Gly			
210 215 220			
Tyr Thr Arg Pro Gln Ser Gly Phe Pro Pro Gly Tyr Leu Ser His Glu			

225		230		235		240									
Ala	Ala	Gly	Lys	Ala	Lys	Leu	Asn	Leu	Met	Gln	Ala	His	Ala	Arg	Ala
		245		250		255									
Tyr	Asp	Ala	Ile	Lys	Glu	His	Ser	Asp	Lys	Pro	Val	Gly	Leu	Ile	Tyr
		260		265		270									
Ser	Phe	Val	Trp	His	Asp	Ala	Leu	Asn	Glu	Glu	Ala	Glu	Glu	Ile	Val
		275		280		285									
Lys	Glu	Ile	Arg	Arg	Arg	His	Tyr	Asp	Phe	Val	Thr	Gly	Leu	His	Ser
		290		295		300									
Gly	Ser	Ser	Glu	Phe	Gly	Glu	Arg	Glu	Asp	Phe	Lys	Gly	Lys	Ile	Asp
305				310		315									320
Trp	Ile	Gly	Val	Asn	Tyr	Tyr	Thr	Arg	Val	Ala	Tyr	Glu	Met	Arg	Asn
		325		330		335									
Gly	Arg	Phe	Met	Ala	Leu	Pro	Gly	Tyr	Gly	Tyr	Met	Cys	Glu	Arg	Ser
		340		345		350									
Gly	Tyr	Ala	Lys	Ser	Gly	Arg	Pro	Ala	Ser	Asp	Phe	Gly	Trp	Glu	Thr
		355		360		365									
Tyr	Pro	Glu	Gly	Leu	Glu	Asn	Val	Leu	Met	Asp	Leu	Lys	Glu	Leu	Tyr
		370		375		380									
Gly	Leu	Pro	Met	Met	Val	Thr	Glu	Asn	Gly	Met	Ala	Asp	Met	Ala	Asp
385				390		395									400
Arg	His	Arg	Ser	Tyr	Tyr	Leu	Val	Ser	His	Leu	Ala	Ala	Ile	His	Arg
		405		410		415									
Ala	Met	Glu	Lys	Gly	Ala	Asp	Val	Arg	Gly	Tyr	Leu	His	Trp	Ser	Leu
		420		425		430									
Thr	Asp	Asn	Tyr	Glu	Trp	Ala	Gln	Gly	Phe	Arg	Met	Arg	Phe	Gly	Leu
		435		440		445									
Val	Met	Val	Asp	Phe	Glu	Thr	Lys	Lys	Arg	Tyr	Ile	Arg	Pro	Ser	Ala
		450		455		460									
Leu	Val	Phe	Arg	Glu	Ile	Ala	Thr	Gln	Lys	Glu	Ile	Pro	Glu	Glu	Leu
465				470		475									480
Ser	His	Leu	Ala	Asn	Leu	Glu	Leu	Val	Thr	Lys	Lys				
		485		490											

<210> 21
 <211> 1455
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> AEPII 1a (clone # 63GA4)

<221> CDS
 <222> (1)...(1455)

<400> 21	
atg aag ttc cca tct aac ttt ctt ttt ggc tac tcc tgg tcg ggc ttc	48
Met Lys Phe Pro Ser Asn Phe Leu Phe Gly Tyr Ser Trp Ser Gly Phe	
1 5 10 15	
cag ttt gaa atg ggt tta cct ggg agt gaa gtt gag agc gac tgg tgg	96
Gln Phe Glu Met Gly Leu Pro Gly Ser Glu Val Glu Ser Asp Trp Trp	
20 25 30	
gca tgg gtc cac gat aag gag aac atc ttc tcg ggc cta gtt agc ggt	144
Ala Trp Val His Asp Lys Glu Asn Ile Phe Ser Gly Leu Val Ser Gly	
35 40 45	
gac cta cca gag aac ggg cct gct tac tgg cac ctc tac aag aaa gac	192
Asp Leu Pro Glu Asn Gly Pro Ala Tyr Trp His Leu Tyr Lys Lys Asp	
50 55 60	

cac gac ata gct gaa agc ctt ggc atg gac gcg ata aga ggc gga atc His Asp Ile Ala Glu Ser Leu Gly Met Asp Ala Ile Arg Gly Gly Ile 65 70 75 80	240
gag tgg gcg agg atc ttc cca aaa ccc acc ttt gac gtg aag gtt gac Glu Trp Ala Arg Ile Phe Pro Lys Pro Thr Phe Asp Val Lys Val Asp 85 90 95	288
gtg gaa aag gac gaa aac ggg aac ata atc tcc att gac gtc ccg gag Val Glu Lys Asp Glu Asn Gly Asn Ile Ile Ser Ile Asp Val Pro Glu 100 105 110	336
agc gcg ata gag gag cta gaa aag ctt gcc aac atg gat gcc ctc aac Ser Ala Ile Glu Glu Leu Glu Lys Leu Ala Asn Met Asp Ala Leu Asn 115 120 125	384
cac tac cgc gaa atc tac tcg gac tgg aag gag agg ggc aag acc ttc His Tyr Arg Glu Ile Tyr Ser Asp Trp Lys Glu Arg Gly Lys Thr Phe 130 135 140	432
ata ttg aac ctc tat cac tgg ccc ctt ccc ctc tgg ctc cac gac ccg Ile Leu Asn Leu Tyr His Trp Pro Leu Pro Leu Trp Leu His Asp Pro 145 150 155 160	480
ata ggc gtt aga aag ctc ggc cct gat aga gct ccc tcg ggc tgg ctg Ile Gly Val Arg Lys Leu Gly Pro Asp Arg Ala Pro Ser Gly Trp Leu 165 170 175	528
gac gag agg agc gtg gtg gag ttc acc aag ttc gct gca ttc atc gcc Asp Glu Arg Ser Val Val Glu Phe Thr Lys Phe Ala Ala Phe Ile Ala 180 185 190	576
tac cac ttg gat gac ctc gtt gac atg tgg agc acg atg aac gag ccg Tyr His Leu Asp Asp Leu Val Asp Met Trp Ser Thr Met Asn Glu Pro 195 200 205	624
aat gtg gtt tac gag cag ggt tac acg agg cct cag tcg ggc ttt cca Asn Val Val Tyr Glu Gln Gly Tyr Thr Arg Pro Gln Ser Gly Phe Pro 210 215 220	672
ccg ggt tat ctc agc cac gag gcc gct gga aag gcg aag ctc aac ctc Pro Gly Tyr Leu Ser His Glu Ala Ala Gly Lys Ala Lys Leu Asn Leu 225 230 235 240	720
atg cag gct cac gct aga gct tac gat gcg ata aaa gag cac tcg gac Met Gln Ala His Ala Arg Ala Tyr Asp Ala Ile Lys Glu His Ser Asp 245 250 255	768
aag cca gtt gga gtt atc tac gca tat aag tgg att gat gcg gag gat Lys Pro Val Gly Val Ile Tyr Ala Tyr Lys Trp Ile Asp Ala Glu Asp 260 265 270	816
gaa gct gca gag gaa tcc gtt ctg gaa ctc cgc agg agg gat tac gac Glu Ala Ala Glu Glu Ser Val Leu Glu Leu Arg Arg Arg Asp Tyr Asp 275 280 285	864
ttc gtt gat ggt ctc tac tca ggc aag tcc ctg act gca ggt gag agg Phe Val Asp Gly Leu Tyr Ser Gly Lys Ser Leu Thr Ala Gly Glu Arg 290 295 300	912

gag gac ttc aaa ggc agg gtc gac tgg gtt ggc gtc aac tac tac tcc	960
Glu Asp Phe Lys Gly Arg Val Asp Trp Val Gly Val Asn Tyr Tyr Ser	
305 310 315 320	
cgc ctg ctc ttt gga aag gcc gga gat tca gtg aga tta ctt gag ggc	1008
Arg Leu Leu Phe Gly Lys Ala Gly Asp Ser Val Arg Leu Leu Glu Gly	
325 330 335	
tac ggt ttt gtc tcc ccg agg ggt ggc tac gcc aaa tcg gga agg cct	1056
Tyr Gly Phe Val Ser Pro Arg Gly Gly Tyr Ala Lys Ser Gly Arg Pro	
340 345 350	
gcg agc gat ttt ggc tgg gag att tat cct gag ggc ctc gaa aag ctc	1104
Ala Ser Asp Phe Gly Trp Glu Ile Tyr Pro Glu Gly Leu Glu Lys Leu	
355 360 365	
ctg gtt gag ctg agt ggc agg tac gag ctt ccg ctc ttc ata acg gag	1152
Leu Val Glu Leu Ser Gly Arg Tyr Glu Leu Pro Leu Phe Ile Thr Glu	
370 375 380	
aat ggt atg gct gat gct gtc gat agg tac agg cct tac tac ctc gtg	1200
Asn Gly Met Ala Asp Ala Val Asp Arg Tyr Arg Pro Tyr Tyr Leu Val	
385 390 395 400	
agc cac ctc gcg gct atc cac agg gcg atg gag aag ggt gcc gac att	1248
Ser His Leu Ala Ala Ile His Arg Ala Met Glu Lys Gly Ala Asp Ile	
405 410 415	
agg ggg tac ctc cac tgg tct ctg acc gac aac tac gag tgg gcg cag	1296
Arg Gly Tyr Leu His Trp Ser Leu Thr Asp Asn Tyr Glu Trp Ala Gln	
420 425 430	
ggc ttc aga atg cgc ttt ggg ctg gtg atg gtg gac ttc gag act aag	1344
Gly Phe Arg Met Arg Phe Gly Leu Val Met Val Asp Phe Glu Thr Lys	
435 440 445	
aag cgc tac ttg agg ccg agc gca ctc gtc ttc agg gaa ata gcc acg	1392
Lys Arg Tyr Leu Arg Pro Ser Ala Leu Val Phe Arg Glu Ile Ala Thr	
450 455 460	
cgg aag gaa ata ccc gaa gag ctt gaa cac ctt gcc gat gtg gat gca	1440
Arg Lys Glu Ile Pro Glu Glu Leu Glu His Leu Ala Asp Val Asp Ala	
465 470 475 480	
atc att gct cgg tga	1455
Ile Ile Ala Arg *	

<210> 22

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> AEPII 1a (clone # 63GP4)

<400> 22

Met Lys Phe Pro Ser Asn Phe Leu Phe Gly Tyr Ser Trp Ser Gly Phe

1

5

10

15

Gln Phe Glu Met Gly Leu Pro Gly Ser Glu Val Glu Ser Asp Trp Trp

<210> 23

<211> 1539
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> AEPII 1a (clone # 63GA9)

<221> CDS
 <222> (1)...(1539)

<400> 23
 atg cta cca gaa gag ttc cta tgg ggc gtt ggg cag tca ggc ttt cag 48
 Met Leu Pro Glu Glu Phe Leu Trp Gly Val Gly Gln Ser Gly Phe Gln
 1 5 10 15

ttc gaa atg ggc gac aag ctc agg agg cac atc gat cca aat acc gac 96
 Phe Glu Met Gly Asp Lys Leu Arg Arg His Ile Asp Pro Asn Thr Asp
 20 25 30

tgg tgg aag tgg gtt cgc gat cct ttc aac ata aaa aag gag ctt gtg 144
 Trp Trp Lys Trp Val Arg Asp Pro Phe Asn Ile Lys Lys Glu Leu Val
 35 40 45

agt ggg gac ctt ccc gag gac ggc atc aac aac tac gaa ctt ttt gaa 192
 Ser Gly Asp Leu Pro Glu Asp Gly Ile Asn Asn Tyr Glu Leu Phe Glu
 50 55 60

aac gat cac aag ctc gct aaa ggc ctt gga ctc aac gca tac agg att 240
 Asn Asp His Lys Leu Ala Lys Gly Leu Gly Leu Asn Ala Tyr Arg Ile
 65 70 75 80

gga ata gag tgg agc aga atc ttt ccc tgg ccg acg tgg acg gtc gat 288
 Gly Ile Glu Trp Ser Arg Ile Phe Pro Trp Pro Thr Trp Thr Val Asp
 85 90 95

acc gag gtc gag ttc gac act tac ggt tta gta aag gac gtt aag ata 336
 Thr Glu Val Glu Phe Asp Thr Tyr Gly Leu Val Lys Asp Val Lys Ile
 100 105 110

gac aag tcc acc ctt gct gaa ctc gac agg ctg gcc aac aag gag gag 384
 Asp Lys Ser Thr Leu Ala Glu Leu Asp Arg Leu Ala Asn Lys Glu Glu
 115 120 125

gta atg tac tac agg cgc gtt att cag cat ttg agg gag ctc ggc ttc 432
 Val Met Tyr Tyr Arg Arg Val Ile Gln His Leu Arg Glu Leu Gly Phe
 130 135 140

aag gtc ttc gtt aac ctc aac cac ttc acg ctt cca ata tgg ctc cac 480
 Lys Val Phe Val Asn Leu Asn His Phe Thr Leu Pro Ile Trp Leu His
 145 150 155 160

gac ccg ata gtg gca agg gag aag gcc ctc aca aac gac aga atc ggc 528
 Asp Pro Ile Val Ala Arg Glu Lys Ala Leu Thr Asn Asp Arg Ile Gly
 165 170 175

tgg gtc tcc cag agg aca gtt gtt gag ttt gcc aag tat gct gct tac 576
 Trp Val Ser Gln Arg Thr Val Val Glu Phe Ala Lys Tyr Ala Ala Tyr
 180 185 190

atc gcc cat gcg ctc gga gac ctc gtg gac aca tgg agc acc ttc aac 624
 Ile Ala His Ala Leu Gly Asp Leu Val Asp Thr Trp Ser Thr Phe Asn

195	200	205	
gaa cct atg gta gtt gtg gag ctc ggc tac ctc gcc ccc tac tca gga Glu Pro Met Val Val Val Glu Leu Gly Tyr Leu Ala Pro Tyr Ser Gly 210 215 220			672
ttt ccc ccg gga gtc atg aac ccc gag gcc gcg aag ctg gcg atc ctc Phe Pro Pro Gly Val Met Asn Pro Glu Ala Lys Leu Ala Ile Leu 225 230 235 240			720
aac atg ata aac gcc cac gcc ttg gca tat aag atg ata aag agg ttc Asn Met Ile Asn Ala His Ala Leu Ala Tyr Lys Met Ile Lys Arg Phe 245 250 255			768
gac acc aag aag gcc gat gag gat agc aag tcc cct gcg gac gtt ggc Asp Thr Lys Lys Ala Asp Glu Asp Ser Lys Ser Pro Ala Asp Val Gly 260 265 270			816
ata atc tac aac aac atc ggt gtt gcc tac cct aaa gac cct aac gat Ile Ile Tyr Asn Asn Ile Gly Val Ala Tyr Pro Lys Asp Pro Asn Asp 275 280 285			864
ccc aag gac gtt aaa gca gcc gaa aac gac aac tac ttc cac agc gga Pro Lys Asp Val Lys Ala Ala Glu Asn Asp Asn Tyr Phe His Ser Gly 290 295 300			912
ctg ttc ttt gat gcc atc cac aag ggt aag ctc aac ata gag ttc gac Leu Phe Phe Asp Ala Ile His Lys Gly Lys Leu Asn Ile Glu Phe Asp 305 310 315 320			960
ggc gaa aac ttt gta aaa gtt aga cac cta aaa ggc aat gac tgg ata Gly Glu Asn Phe Val Lys Val Arg His Leu Lys Gly Asn Asp Trp Ile 325 330 335			1008
ggc ctc aac tac tac acc cgc gag gtt gtt aga tat tcg gag ccc aag Gly Leu Asn Tyr Tyr Thr Arg Glu Val Val Arg Tyr Ser Glu Pro Lys 340 345 350			1056
ttc cca agt ata ccc ctc ata tcc ttc aag ggc gtt ccc aac tac ggc Phe Pro Ser Ile Pro Leu Ile Ser Phe Lys Gly Val Pro Asn Tyr Gly 355 360 365			1104
tac tcc tgc agg ccc ggc acg acc tcc gcc gat ggc atg ccc gtc agc Tyr Ser Cys Arg Pro Gly Thr Thr Ser Ala Asp Gly Met Pro Val Ser 370 375 380			1152
gat atc ggc tgg gaa gtc tat ccc cag gga atc tac gac tcg ata gtc Asp Ile Gly Trp Glu Val Tyr Pro Gln Gly Ile Tyr Asp Ser Ile Val 385 390 395 400			1200
gag gcc acc aag tac agt gtt cct gtt tac gtc acc gag aac ggt gtt Glu Ala Thr Lys Tyr Ser Val Pro Val Tyr Val Thr Glu Asn Gly Val 405 410 415			1248
gcg gat tcc gcg gac acg ctg agg cca tac tac ata gtc agc cac gtc Ala Asp Ser Ala Asp Thr Leu Arg Pro Tyr Tyr Ile Val Ser His Val 420 425 430			1296
tca aag ata gag gaa gcc att gag aat gga tac ccc gta aaa ggc tac Ser Lys Ile Glu Glu Ala Ile Glu Asn Gly Tyr Pro Val Lys Gly Tyr 435 440 445			1344

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atg tac tgg gcg ctt acg gat aac tac gag tgg gcc ctc ggc ttc agc      1392
Met Tyr Trp Ala Leu Thr Asp Asn Tyr Glu Trp Ala Leu Gly Phe Ser
  450                      455                      460

atg agg ttt ggt ctc tac aag gtc gac ctc atc tcc aag gag agg atc      1440
Met Arg Phe Gly Leu Tyr Lys Val Asp Leu Ile Ser Lys Glu Arg Ile
  465                      470                      475                      480

ccg agg gag aga agc gtt gag ata tat cgc agg ata gtg cag tcc aac      1488
Pro Arg Glu Arg Ser Val Glu Ile Tyr Arg Arg Ile Val Gln Ser Asn
          485                      490                      495

ggt gtt cct aag gat atc aaa gag gag ttc ctg aag ggt gag gag aaa      1536
Gly Val Pro Lys Asp Ile Lys Glu Glu Phe Leu Lys Gly Glu Glu Lys
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tga
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<210> 24
<211> 512
<212> PRT
<213> Artificial Sequence

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<220>
<223> AEPII 1a (clone # 63GP4)

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  20          25          30
Trp Trp Lys Trp Val Arg Asp Pro Phe Asn Ile Lys Lys Glu Leu Val
  35          40          45
Ser Gly Asp Leu Pro Glu Asp Gly Ile Asn Asn Tyr Glu Leu Phe Glu
  50          55          60
Asn Asp His Lys Leu Ala Lys Gly Leu Gly Leu Asn Ala Tyr Arg Ile
  65          70          75          80
Gly Ile Glu Trp Ser Arg Ile Phe Pro Trp Pro Thr Trp Thr Val Asp
  85          90          95
Thr Glu Val Glu Phe Asp Thr Tyr Gly Leu Val Lys Asp Val Lys Ile
  100         105         110
Asp Lys Ser Thr Leu Ala Glu Leu Asp Arg Leu Ala Asn Lys Glu Glu
  115         120         125
Val Met Tyr Tyr Arg Arg Val Ile Gln His Leu Arg Glu Leu Gly Phe
  130         135         140
Lys Val Phe Val Asn Leu Asn His Phe Thr Leu Pro Ile Trp Leu His
  145         150         155         160
Asp Pro Ile Val Ala Arg Glu Lys Ala Leu Thr Asn Asp Arg Ile Gly
  165         170         175
Trp Val Ser Gln Arg Thr Val Val Glu Phe Ala Lys Tyr Ala Ala Tyr
  180         185         190
Ile Ala His Ala Leu Gly Asp Leu Val Asp Thr Trp Ser Thr Phe Asn
  195         200         205
Glu Pro Met Val Val Val Glu Leu Gly Tyr Leu Ala Pro Tyr Ser Gly
  210         215         220
Phe Pro Pro Gly Val Met Asn Pro Glu Ala Ala Lys Leu Ala Ile Leu
  225         230         235         240

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Asn Met Ile Asn Ala His Ala Leu Ala Tyr Lys Met Ile Lys Arg Phe
      245      250      255
Asp Thr Lys Lys Ala Asp Glu Asp Ser Lys Ser Pro Ala Asp Val Gly
      260      265      270
Ile Ile Tyr Asn Asn Ile Gly Val Ala Tyr Pro Lys Asp Pro Asn Asp
      275      280      285
Pro Lys Asp Val Lys Ala Ala Glu Asn Asp Asn Tyr Phe His Ser Gly
      290      295      300
Leu Phe Phe Asp Ala Ile His Lys Gly Lys Leu Asn Ile Glu Phe Asp
305      310      315      320
Gly Glu Asn Phe Val Lys Val Arg His Leu Lys Gly Asn Asp Trp Ile
      325      330      335
Gly Leu Asn Tyr Tyr Thr Arg Glu Val Val Arg Tyr Ser Glu Pro Lys
      340      345      350
Phe Pro Ser Ile Pro Leu Ile Ser Phe Lys Gly Val Pro Asn Tyr Gly
      355      360      365
Tyr Ser Cys Arg Pro Gly Thr Thr Ser Ala Asp Gly Met Pro Val Ser
      370      375      380
Asp Ile Gly Trp Glu Val Tyr Pro Gln Gly Ile Tyr Asp Ser Ile Val
385      390      395      400
Glu Ala Thr Lys Tyr Ser Val Pro Val Tyr Val Thr Glu Asn Gly Val
      405      410      415
Ala Asp Ser Ala Asp Thr Leu Arg Pro Tyr Tyr Ile Val Ser His Val
      420      425      430
Ser Lys Ile Glu Glu Ala Ile Glu Asn Gly Tyr Pro Val Lys Gly Tyr
      435      440      445
Met Tyr Trp Ala Leu Thr Asp Asn Tyr Glu Trp Ala Leu Gly Phe Ser
      450      455      460
Met Arg Phe Gly Leu Tyr Lys Val Asp Leu Ile Ser Lys Glu Arg Ile
465      470      475      480
Pro Arg Glu Arg Ser Val Glu Ile Tyr Arg Arg Ile Val Gln Ser Asn
      485      490      495
Gly Val Pro Lys Asp Ile Lys Glu Glu Phe Leu Lys Gly Glu Glu Lys
      500      505      510

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<210> 25
 <211> 1539
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> AEPII 1a (clone # 63GB1)

<221> CDS
 <222> (1)...(1536)

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<400> 25
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  1              5              10              15

ttc gaa atg ggc gac aag ctc agg agg cac atc gat cca aat acc gac      96
Phe Glu Met Gly Asp Lys Leu Arg Arg His Ile Asp Pro Asn Thr Asp
      20              25              30

tgg tgg aag tgg gtt cgc gat cct ttc aac ata aaa aag gag ctt gtg      144
Trp Trp Lys Trp Val Arg Asp Pro Phe Asn Ile Lys Lys Glu Leu Val
      35              40              45

agt ggg gac ctt ccc gag gac ggc atc aac aac tac gaa ctt ttt gaa      192
Ser Gly Asp Leu Pro Glu Asp Gly Ile Asn Asn Tyr Glu Leu Phe Glu

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50	55	60	
aac gat cac aag ctc gct aaa ggc ctt gga ctc aac gca tac ggg att Asn Asp His Lys Leu Ala Lys Gly Leu Gly Leu Asn Ala Tyr Gly Ile 65 70 75 80			240
gga ata gag tgg agc aga atc ttt ccc tgg ccg acg tgg acg gtc gat Gly Ile Glu Trp Ser Arg Ile Phe Pro Trp Pro Thr Trp Thr Val Asp 85 90 95			288
acc gag gtc gag ttc gac act tac ggt tta gta aag gac gtt aag ata Thr Glu Val Glu Phe Asp Thr Tyr Gly Leu Val Lys Asp Val Lys Ile 100 105 110			336
gac aag tcc acc ctt gct gaa ctc gac agg ctg gcc aac aag gag gag Asp Lys Ser Thr Leu Ala Glu Leu Asp Arg Leu Ala Asn Lys Glu Glu 115 120 125			384
gta atg tac tac agg cgc gtt att cag cat ttg agg gag ctc ggc ttc Val Met Tyr Tyr Arg Arg Val Ile Gln His Leu Arg Glu Leu Gly Phe 130 135 140			432
aag gtc ttc gtt aac ctc aac cac ttc acg ctt cca ata tgg ctc cac Lys Val Phe Val Asn Leu Asn His Phe Thr Leu Pro Ile Trp Leu His 145 150 155 160			480
gac ccg ata gtg gca agg gag aag gcc ctc aca aac gac aga atc ggc Asp Pro Ile Val Ala Arg Glu Lys Ala Leu Thr Asn Asp Arg Ile Gly 165 170 175			528
tgg gtc tcc cag agg aca gtt gtt gag ttt gcc aag tat gct gct tac Trp Val Ser Gln Arg Thr Val Val Glu Phe Ala Lys Tyr Ala Ala Tyr 180 185 190			576
atc gcc cat gcg ctc gga gac ctc gtg gac aca tgg agc acc ttc aac Ile Ala His Ala Leu Gly Asp Leu Val Asp Thr Trp Ser Thr Phe Asn 195 200 205			624
gaa cct atg gta gtt gtg gag ctc gga tac ctc gcc ccc tac tca gga Glu Pro Met Val Val Val Glu Leu Gly Tyr Leu Ala Pro Tyr Ser Gly 210 215 220			672
ttt ccc ccg gga gtc atg aac ccc gag gcc gcg aag ctg gcg atc ctc Phe Pro Pro Gly Val Met Asn Pro Glu Ala Ala Lys Leu Ala Ile Leu 225 230 235 240			720
aac atg ata aac gcc cac gcc ttg gca tat aag atg ata aag agg ttc Asn Met Ile Asn Ala His Ala Leu Ala Tyr Lys Met Ile Lys Arg Phe 245 250 255			768
gac acc aag aag gcc gat gag gat agc aag tcc cct gcg gac gtt ggc Asp Thr Lys Lys Ala Asp Glu Asp Ser Lys Ser Pro Ala Asp Val Gly 260 265 270			816
ata atc tac aac aac atc ggt gtt gcc tac cct aaa gac cct aac gat Ile Ile Tyr Asn Asn Ile Gly Val Ala Tyr Pro Lys Asp Pro Asn Asp 275 280 285			864
ccc aag gac gtt aaa gca gcc gaa aac gac aac tac ttc cac agc gga Pro Lys Asp Val Lys Ala Ala Glu Asn Asp Asn Tyr Phe His Ser Gly 290 295 300			912

ctg ttc ttt gat gcc atc cac aag ggt aag ctc aac ata gag ttc gac Leu Phe Phe Asp Ala Ile His Lys Gly Lys Leu Asn Ile Glu Phe Asp 305 310 315 320	960
ggc gaa aac ttt gta aaa gtt aga cac cta aaa ggc aat gac tgg ata Gly Glu Asn Phe Val Lys Val Arg His Leu Lys Gly Asn Asp Trp Ile 325 330 335	1008
ggc ctc aac tac tac acc cgc gag gtt gtt aga tat tcg gag ccc aag Gly Leu Asn Tyr Tyr Thr Arg Glu Val Val Arg Tyr Ser Glu Pro Lys 340 345 350	1056
ttc cca agt ata ccc ctc ata tcc ttc aag ggc gtt ccc aac tac ggc Phe Pro Ser Ile Pro Leu Ile Ser Phe Lys Gly Val Pro Asn Tyr Gly 355 360 365	1104
tac tcc tgc agg ccc ggc acg acc tcc gcc gat ggc atg ccc gtc agc Tyr Ser Cys Arg Pro Gly Thr Thr Ser Ala Asp Gly Met Pro Val Ser 370 375 380	1152
gat atc ggc tgg gaa gtc tat ccc cag gga atc tac gac tcg ata gtc Asp Ile Gly Trp Glu Val Tyr Pro Gln Gly Ile Tyr Asp Ser Ile Val 385 390 395 400	1200
gag gcc acc aag tac agt gtt cct gtt tac gtc acc gag aac ggt gtt Glu Ala Thr Lys Tyr Ser Val Pro Val Tyr Val Thr Glu Asn Gly Val 405 410 415	1248
gcg gat tcc gcg gac acg ctg agg cca tac tac ata gtc agc cac gtc Ala Asp Ser Ala Asp Thr Leu Arg Pro Tyr Tyr Ile Val Ser His Val 420 425 430	1296
tca aag ata gag gaa gcc att gag aat gga tac ccc gta aaa ggc tac Ser Lys Ile Glu Glu Ala Ile Glu Asn Gly Tyr Pro Val Lys Gly Tyr 435 440 445	1344
atg tac tgg gcg ctt acg gat aac tac gag tgg gcc ctc ggc ttc agc Met Tyr Trp Ala Leu Thr Asp Asn Tyr Glu Trp Ala Leu Gly Phe Ser 450 455 460	1392
atg agg ttt ggt ctc tac aag gtc gac ctc atc tcc aag gag agg atc Met Arg Phe Gly Leu Tyr Lys Val Asp Leu Ile Ser Lys Glu Arg Ile 465 470 475 480	1440
ccg agg gag aga agc gtt gag ata tat cgc agg ata gtg cag tcc aac Pro Arg Glu Arg Ser Val Glu Ile Tyr Arg Arg Ile Val Gln Ser Asn 485 490 495	1488
ggt gtt cct aag gat atc aaa gag gag ttc ctg aag ggt gag gag aaa Gly Val Pro Lys Asp Ile Lys Glu Glu Phe Leu Lys Gly Glu Glu Lys 500 505 510	1536
tga	1539
<210> 26	
<211> 512	
<212> PRT	
<213> Artificial Sequence	
<220>	

<223> AEP11 1a (clone # 63GP4)

<400> 26

Met	Leu	Pro	Glu	Glu	Phe	Leu	Trp	Gly	Val	Gly	Gln	Ser	Gly	Phe	Gln
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Phe	Glu	Met	Gly	Asp	Lys	Leu	Arg	Arg	His	Ile	Asp	Pro	Asn	Thr	Asp
		20					25						30		
Trp	Trp	Lys	Trp	Val	Arg	Asp	Pro	Phe	Asn	Ile	Lys	Lys	Glu	Leu	Val
		35					40					45			
Ser	Gly	Asp	Leu	Pro	Glu	Asp	Gly	Ile	Asn	Asn	Tyr	Glu	Leu	Phe	Glu
	50					55					60				
Asn	Asp	His	Lys	Leu	Ala	Lys	Gly	Leu	Gly	Leu	Asn	Ala	Tyr	Gly	Ile
65					70					75					80
Gly	Ile	Glu	Trp	Ser	Arg	Ile	Phe	Pro	Trp	Pro	Thr	Trp	Thr	Val	Asp
				85					90					95	
Thr	Glu	Val	Glu	Phe	Asp	Thr	Tyr	Gly	Leu	Val	Lys	Asp	Val	Lys	Ile
			100					105					110		
Asp	Lys	Ser	Thr	Leu	Ala	Glu	Leu	Asp	Arg	Leu	Ala	Asn	Lys	Glu	Glu
		115					120					125			
Val	Met	Tyr	Tyr	Arg	Arg	Val	Ile	Gln	His	Leu	Arg	Glu	Leu	Gly	Phe
	130					135					140				
Lys	Val	Phe	Val	Asn	Leu	Asn	His	Phe	Thr	Leu	Pro	Ile	Trp	Leu	His
145					150					155					160
Asp	Pro	Ile	Val	Ala	Arg	Glu	Lys	Ala	Leu	Thr	Asn	Asp	Arg	Ile	Gly
				165					170					175	
Trp	Val	Ser	Gln	Arg	Thr	Val	Val	Glu	Phe	Ala	Lys	Tyr	Ala	Ala	Tyr
		180						185					190		
Ile	Ala	His	Ala	Leu	Gly	Asp	Leu	Val	Asp	Thr	Trp	Ser	Thr	Phe	Asn
		195					200					205			
Glu	Pro	Met	Val	Val	Val	Glu	Leu	Gly	Tyr	Leu	Ala	Pro	Tyr	Ser	Gly
	210					215					220				
Phe	Pro	Pro	Gly	Val	Met	Asn	Pro	Glu	Ala	Ala	Lys	Leu	Ala	Ile	Leu
225					230				235						240
Asn	Met	Ile	Asn	Ala	His	Ala	Leu	Ala	Tyr	Lys	Met	Ile	Lys	Arg	Phe
				245					250					255	
Asp	Thr	Lys	Lys	Ala	Asp	Glu	Asp	Ser	Lys	Ser	Pro	Ala	Asp	Val	Gly
		260						265					270		
Ile	Ile	Tyr	Asn	Asn	Ile	Gly	Val	Ala	Tyr	Pro	Lys	Asp	Pro	Asn	Asp
		275					280					285			
Pro	Lys	Asp	Val	Lys	Ala	Ala	Glu	Asn	Asp	Asn	Tyr	Phe	His	Ser	Gly
	290					295					300				
Leu	Phe	Phe	Asp	Ala	Ile	His	Lys	Gly	Lys	Leu	Asn	Ile	Glu	Phe	Asp
305					310					315					320
Gly	Glu	Asn	Phe	Val	Lys	Val	Arg	His	Leu	Lys	Gly	Asn	Asp	Trp	Ile
				325					330					335	
Gly	Leu	Asn	Tyr	Thr	Arg	Glu	Val	Val	Arg	Tyr	Ser	Glu	Pro	Lys	
		340					345					350			
Phe	Pro	Ser	Ile	Pro	Leu	Ile	Ser	Phe	Lys	Gly	Val	Pro	Asn	Tyr	Gly
		355					360					365			
Tyr	Ser	Cys	Arg	Pro	Gly	Thr	Thr	Ser	Ala	Asp	Gly	Met	Pro	Val	Ser
	370					375					380				
Asp	Ile	Gly	Trp	Glu	Val	Tyr	Pro	Gln	Gly	Ile	Tyr	Asp	Ser	Ile	Val
385					390					395					400
Glu	Ala	Thr	Lys	Tyr	Ser	Val	Pro	Val	Tyr	Val	Thr	Glu	Asn	Gly	Val
				405					410					415	
Ala	Asp	Ser	Ala	Asp	Thr	Leu	Arg	Pro	Tyr	Tyr	Ile	Val	Ser	His	Val
			420					425				430			
Ser	Lys	Ile	Glu	Glu	Ala	Ile	Glu	Asn	Gly	Tyr	Pro	Val	Lys	Gly	Tyr
		435					440					445			
Met	Tyr	Trp	Ala	Leu	Thr	Asp	Asn	Tyr	Glu	Trp	Ala	Leu	Gly	Phe	Ser
	450					455					460				

Met Arg Phe Gly Leu Tyr Lys Val Asp Leu Ile Ser Lys Glu Arg Ile
 465 470 475 480
 Pro Arg Glu Arg Ser Val Glu Ile Tyr Arg Arg Ile Val Gln Ser Asn
 485 490 495
 Gly Val Pro Lys Asp Ile Lys Glu Glu Phe Leu Lys Gly Glu Glu Lys
 500 505 510

<210> 27
 <211> 1575
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> AEPII 1a (clone # 63GP1)

<221> CDS
 <222> (1)...(1572)

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 tac ctc caa cgt aac ata aag aca caa aac caa tat tgg gca ttg tgc 96
 Tyr Leu Gln Arg Asn Ile Lys Thr Gln Asn Gln Tyr Trp Ala Leu Cys
 20 25 30
 gta gta atg ttc tcc aat gtt ctt aga tgg caa aac tta aat att tca 144
 Val Val Met Phe Ser Asn Val Leu Arg Trp Gln Asn Leu Asn Ile Ser
 35 40 45
 cca gcg gtg ata cat aga gac acc gct gaa cac aga ggt gat tcc atg 192
 Pro Ala Val Ile His Arg Asp Thr Ala Glu His Arg Gly Asp Ser Met
 50 55 60
 aag aag ttt gtc gcc ctg ttc ata acc atg ttt ttc gta gtg agc atg 240
 Lys Lys Phe Val Ala Leu Phe Ile Thr Met Phe Phe Val Val Ser Met
 65 70 75 80
 gca gtc gtt gca cag cca gct agc gcc gca aag tat tcc gag ctc gaa 288
 Ala Val Val Ala Gln Pro Ala Ser Ala Ala Lys Tyr Ser Glu Leu Glu
 85 90 95
 gaa ggc ggc gtt ata atg cag gcc ttc tac tgg gac gtc cca ggt gga 336
 Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Gly Gly
 100 105 110
 gga atc tgg tgg gac acc atc agg agc aag ata ccg gag tgg tac gag 384
 Gly Ile Trp Trp Asp Thr Ile Arg Ser Lys Ile Pro Glu Trp Tyr Glu
 115 120 125
 gcg gga ata tcc gcc att tgg att ccg cca gcc agc aag ggg atg agc 432
 Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met Ser
 130 135 140
 ggc ggt tac tcg atg ggc tac gat ccc tac gat ttc ttt gac ctc ggc 480
 Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu Gly
 145 150 155 160
 gag tac aac cag aag gga acc atc gaa acg cgc ttt ggc tct aaa cag 528
 Glu Tyr Asn Gln Lys Gly Thr Ile Glu Thr Arg Phe Gly Ser Lys Gln

165	170	175	
gag ctc atc aat atg ata aac acg gcc cat gcc tac ggc ata aag gtc Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys Val 180 185 190			576
ata gcg gac atc gtc ata aac cac cgc gca ggc gga gac ctc gag tgg Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu Trp 195 200 205			624
aac ccg ttc gtt ggg gac tac acc tgg acg gac ttc tca aag gtg gcc Asn Pro Phe Val Gly Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala 210 215 220			672
tcg ggc aaa tat act gcc aac tac ctc gac ttc cac ccc aac gag gtc Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu Val 225 230 235 240			720
aag tgc tgt gac gag ggc aca ttt gga ggc ttc cca gac ata gcc cac Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala His 245 250 255			768
gag aag agc tgg gac cag cac tgg ctc tgg gcg agc gat gag agc tac Glu Lys Ser Trp Asp Gln His Trp Leu Trp Ala Ser Asp Glu Ser Tyr 260 265 270			816
gcc gcc tac cta agg agc atc ggc gtt gat gcc tgg cgc ttt gac tac Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp Tyr 275 280 285			864
gtg aag ggc tac gga gcg tgg gtc gtc aag gac tgg ctc aac tgg tgg Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asn Trp Trp 290 295 300			912
ggc ggc tgg gcc gtt ggc gag tac tgg gac acc aac gtt gat gca ctc Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu 305 310 315 320			960
ctc aac tgg gcc tac tcg agc ggc gcc aag gtc ttc gac ttc ccg ctc Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe Pro Leu 325 330 335			1008
tac tac aag atg gat gag gcc ttt gac aac aaa aac att cca gcg ctc Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu 340 345 350			1056
gtc tct gcc ctt cag aac ggc cag act gtt gtc tcc cgc gac ccg ttc Val Ser Ala Leu Gln Asn Gly Gln Thr Val Val Ser Arg Asp Pro Phe 355 360 365			1104
aag gcc gta acc ttt gta gca aac cac gac acc gat ata atc tgg aac Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp Asn 370 375 380			1152
aag tac ctt gct tat gct ttc atc ctc acc tac gaa ggc cag ccc gtc Lys Tyr Leu Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro Val 385 390 395 400			1200
ata ttt tac cgc gac tac gag gag tgg ctc aac aag gac agg ttg aac Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu Asn 405 410 415			1248

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aac ctc ata tgg ata cac gac cac ctc gca ggt gga agc acg agc ata      1296
Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Ser Ile
      420                      425                      430

gtt tac tac gac agc gac gag atg att ttc gtg agg aac ggc tat gga      1344
Val Tyr Tyr Asp Ser Asp Glu Met Ile Phe Val Arg Asn Gly Tyr Gly
      435                      440                      445

agc aag cct ggc ctt ata act tac atc aac ctc ggc tcg agc aag gtt      1392
Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val
      450                      455                      460

gga agg tgg gtt tat gtg ccg aag ttc gcg ggc gcg tgc atc cac gag      1440
Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His Glu
      465                      470                      475                      480

tat act ggt aac ctc gga ggc tgg gta gac aag tac gtc tac tca agc      1488
Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser
      485                      490                      495

ggc tgg gtc tat ttc gaa gct cca gct tac gac cct gcc aac ggg cag      1536
Gly Trp Val Tyr Phe Glu Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln
      500                      505                      510

tat ggc tac tcc gtg tgg agc tat tgc ggt gtt ggg tga      1575
Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
      515                      520

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<210> 28

<211> 524

<212> PRT

<213> Artificial Sequence

<220>

<223> AEPII 1a (clone # 63GP4)

<400> 28

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Met Arg Pro Phe Leu Leu Ile Ser Ile Leu Asp Phe Arg Val Ala Asp
 1           5           10           15
Tyr Leu Gln Arg Asn Ile Lys Thr Gln Asn Gln Tyr Trp Ala Leu Cys
      20           25           30
Val Val Met Phe Ser Asn Val Leu Arg Trp Gln Asn Leu Asn Ile Ser
      35           40           45
Pro Ala Val Ile His Arg Asp Thr Ala Glu His Arg Gly Asp Ser Met
      50           55           60
Lys Lys Phe Val Ala Leu Phe Ile Thr Met Phe Phe Val Val Ser Met
      65           70           75           80
Ala Val Val Ala Gln Pro Ala Ser Ala Ala Lys Tyr Ser Glu Leu Glu
      85           90           95
Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Gly Gly
      100          105          110
Gly Ile Trp Trp Asp Thr Ile Arg Ser Lys Ile Pro Glu Trp Tyr Glu
      115          120          125
Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met Ser
      130          135          140
Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu Gly
      145          150          155          160
Glu Tyr Asn Gln Lys Gly Thr Ile Glu Thr Arg Phe Gly Ser Lys Gln
      165          170          175

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Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys Val
 180 185 190
 Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu Trp
 195 200 205
 Asn Pro Phe Val Gly Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala
 210 215 220
 Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu Val
 225 230 235 240
 Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala His
 245 250 255
 Glu Lys Ser Trp Asp Gln His Trp Leu Trp Ala Ser Asp Glu Ser Tyr
 260 265 270
 Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp Tyr
 275 280 285
 Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asn Trp Trp
 290 295 300
 Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu
 305 310 315 320
 Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe Pro Leu
 325 330 335
 Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu
 340 345 350
 Val Ser Ala Leu Gln Asn Gly Gln Thr Val Val Ser Arg Asp Pro Phe
 355 360 365
 Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp Asn
 370 375 380
 Lys Tyr Leu Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro Val
 385 390 395 400
 Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu Asn
 405 410 415
 Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Ser Ile
 420 425 430
 Val Tyr Tyr Asp Ser Asp Glu Met Ile Phe Val Arg Asn Gly Tyr Gly
 435 440 445
 Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val
 450 455 460
 Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His Glu
 465 470 475 480
 Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser
 485 490 495
 Gly Trp Val Tyr Phe Glu Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln
 500 505 510
 Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
 515 520

<210> 29
 <211> 1887
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> AEPII 1a (clone # 63GP2)

<221> CDS
 <222> (1)...(1884)

<400> 29
 atg ata aac gtt gca acg gga gag gag acc cca ata cac ctc ttt gga
 Met Ile Asn Val Ala Thr Gly Glu Glu Thr Pro Ile His Leu Phe Gly
 1 5 10 15

gtc aac tgg ttc ggc ttt gag aca ccg aac tac gtt gtt cac ggc cta Val Asn Trp Phe Gly Phe Glu Thr Pro Asn Tyr Val Val His Gly Leu 20 25 30	96
tgg agt agg aac tgg gag gac atg ctc ctc cag atc aag agc ctt ggc Trp Ser Arg Asn Trp Glu Asp Met Leu Leu Gln Ile Lys Ser Leu Gly 35 40 45	144
ttc aat gcg ata agg ctt ccc ttc tgt acc cag tca gta aaa ccg ggg Phe Asn Ala Ile Arg Leu Pro Phe Cys Thr Gln Ser Val Lys Pro Gly 50 55 60	192
acg atg cca acg gcg att gac tac gcc aag aac cca gac ctc cag ggt Thr Met Pro Thr Ala Ile Asp Tyr Ala Lys Asn Pro Asp Leu Gln Gly 65 70 75 80	240
ctt gac agc gtc cag ata atg gag aaa ata atc aag aag gct gga gac Leu Asp Ser Val Gln Ile Met Glu Lys Ile Ile Lys Lys Ala Gly Asp 85 90 95	288
ctg ggc ata ttc gtg ctc ctc gac tac cac aga ata gga tgc aac ttc Leu Gly Ile Phe Val Leu Leu Asp Tyr His Arg Ile Gly Cys Asn Phe 100 105 110	336
ata gaa ccc cta tgg tac acc gac agc ttc tcg gag cag gac tac ata Ile Glu Pro Leu Trp Tyr Thr Asp Ser Phe Ser Glu Gln Asp Tyr Ile 115 120 125	384
aac acc tgg gtt gaa gtc gcc cag agg ttc ggc aag tac tgg aac gtt Asn Thr Trp Val Glu Val Ala Gln Arg Phe Gly Lys Tyr Trp Asn Val 130 135 140	432
atc ggc gcg gac ctg aag aac gaa ccc cac agc tca agc ccc gca cct Ile Gly Ala Asp Leu Lys Asn Glu Pro His Ser Ser Ser Pro Ala Pro 145 150 155 160	480
gcc gcc tac act gac gga agt ggg gcc acg tgg gga atg ggc aac aac Ala Ala Tyr Thr Asp Gly Ser Gly Ala Thr Trp Gly Met Gly Asn Asn 165 170 175	528
gcc acc gac tgg aac ctg gcg gct gag agg ata gga agg gca att ctg Ala Thr Asp Trp Asn Leu Ala Ala Glu Arg Ile Gly Arg Ala Ile Leu 180 185 190	576
gag gtt gcc cca caa tgg gtt ata ttt gtt gag gga acc cag ttc acc Glu Val Ala Pro Gln Trp Val Ile Phe Val Glu Gly Thr Gln Phe Thr 195 200 205	624
acc ccc gag ata gac ggt agg tac aag tgg ggc cac aac gcc tgg tgg Thr Pro Glu Ile Asp Gly Arg Tyr Lys Trp Gly His Asn Ala Trp Trp 210 215 220	672
ggc gga aac ctt atg ggt gtt agg aag tac cca gtt aac ctg ccc agg Gly Gly Asn Leu Met Gly Val Arg Lys Tyr Pro Val Asn Leu Pro Arg 225 230 235 240	720
gac aag ctt gtt tac agc ccc caa gtt tac ggt cca gac gtt tac gac Asp Lys Leu Val Tyr Ser Pro Gln Val Tyr Gly Pro Asp Val Tyr Asp 245 250 255	768
cag ccc tac ttt gac ccc ggt gag ggg ttc ccc gac aac ctc ccc gaa	816

Gln	Pro	Tyr	Phe	Asp	Pro	Gly	Glu	Gly	Phe	Pro	Asp	Asn	Leu	Pro	Glu	
			260					265					270			
ata	tgg	tac	cac	cac	ttc	ggc	tac	gta	aag	ctt	gat	ctc	ggg	tac	cct	864
Ile	Trp	Tyr	His	His	Phe	Gly	Tyr	Val	Lys	Leu	Asp	Leu	Gly	Tyr	Pro	
		275					280					285				
gtt	gtt	ata	ggg	gag	ttc	gga	ggc	aag	tac	ggc	cat	ggg	gga	gac	ccg	912
Val	Val	Ile	Gly	Glu	Phe	Gly	Gly	Lys	Tyr	Gly	His	Gly	Gly	Asp	Pro	
	290					295					300					
agg	gat	gtc	act	tgg	cag	aac	aag	ata	ata	gac	tgg	atg	atc	cag	aac	960
Arg	Asp	Val	Thr	Trp	Gln	Asn	Lys	Ile	Ile	Asp	Trp	Met	Ile	Gln	Asn	
305					310					315				320		
aaa	ttc	tgt	gac	ttc	ttc	tac	tgg	agc	tgg	aac	cca	aac	agc	ggg	gac	1008
Lys	Phe	Cys	Asp	Phe	Phe	Tyr	Trp	Ser	Trp	Asn	Pro	Asn	Ser	Gly	Asp	
				325					330					335		
acc	ggg	gga	att	ctg	aag	gat	gac	tgg	acg	aca	ata	tgg	gag	gac	aag	1056
Thr	Gly	Gly	Ile	Leu	Lys	Asp	Asp	Trp	Thr	Thr	Ile	Trp	Glu	Asp	Lys	
			340					345					350			
tac	aac	aac	ctg	aag	agg	ctc	atg	gac	agc	tgt	tct	gga	aac	gcc	act	1104
Tyr	Asn	Asn	Leu	Lys	Arg	Leu	Met	Asp	Ser	Cys	Ser	Gly	Asn	Ala	Thr	
		355					360					365				
gcc	ccg	tcc	gtc	ccc	acg	aca	act	aca	aca	aca	agc	aca	ccg	cca	acg	1152
Ala	Pro	Ser	Val	Pro	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Pro	Pro	Thr	
	370					375					380					
acc	aca	acg	act	aca	aca	tcc	act	cca	acg	acc	act	acc	cag	acc	ccg	1200
Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Pro	Thr	Thr	Thr	Thr	Gln	Thr	Pro	
385					390					395				400		
acc	acc	act	act	cca	act	acg	aca	acc	acc	acg	acc	aca	act	cct	tca	1248
Thr	Thr	Thr	Thr	Pro	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Pro	Ser	
				405					410					415		
aat	aac	gtc	cca	ttt	gaa	att	gtg	aac	gtt	ctc	ccg	act	agc	tcc	cag	1296
Asn	Asn	Val	Pro	Phe	Glu	Ile	Val	Asn	Val	Leu	Pro	Thr	Ser	Ser	Gln	
		420						425				430				
tac	gag	gga	acc	agc	gtg	gag	gtt	gta	tgt	gat	gga	acc	cag	tgt	gcc	1344
Tyr	Glu	Gly	Thr	Ser	Val	Glu	Val	Val	Cys	Asp	Gly	Thr	Gln	Cys	Ala	
		435					440					445				
tcc	agc	gtt	tgg	gga	gct	ccg	aac	ctc	tgg	gga	gtc	gtt	aaa	atc	gga	1392
Ser	Ser	Val	Trp	Gly	Ala	Pro	Asn	Leu	Trp	Gly	Val	Val	Lys	Ile	Gly	
	450					455					460					
aac	gcc	acc	atg	gac	ccc	aac	gtt	tgg	ggc	tgg	gag	gac	gtt	tac	aag	1440
Asn	Ala	Thr	Met	Asp	Pro	Asn	Val	Trp	Gly	Trp	Glu	Asp	Val	Tyr	Lys	
465					470				475					480		
act	gca	ccc	cag	gac	att	gga	acc	ggc	agc	aca	aag	atg	gag	ata	agg	1488
Thr	Ala	Pro	Gln	Asp	Ile	Gly	Thr	Gly	Ser	Thr	Lys	Met	Glu	Ile	Arg	
				485				490					495			
aac	ggg	gtg	ctc	aag	gtt	aca	aac	ctc	tgg	aac	atc	aac	atg	cat	ccg	1536
Asn	Gly	Val	Leu	Lys	Val	Thr	Asn	Leu	Trp	Asn	Ile	Asn	Met	His	Pro	

500	505	510	
aag tat aac aca atg gca tac ccg gag gtc ata tac ggc gcc aag cct Lys Tyr Asn Thr Met Ala Tyr Pro Glu Val Ile Tyr Gly Ala Lys Pro 515 520 525			1584
tgg ggc aac cag cca ata aac gct ccg aac ttc gtg ctc ccg ata aag Trp Gly Asn Gln Pro Ile Asn Ala Pro Asn Phe Val Leu Pro Ile Lys 530 535 540			1632
gtc tcc cag ctt ccg agg ata ctc gtt gac aca aag tac acg ctc gaa Val Ser Gln Leu Pro Arg Ile Leu Val Asp Thr Lys Tyr Thr Leu Glu 545 550 555 560			1680
aag agc ttc ccg gga aac aac ttc gcc ttt gag gcc tgg ctc ttc aag Lys Ser Phe Pro Gly Asn Asn Phe Ala Phe Glu Ala Trp Leu Phe Lys 565 570 575			1728
gat gcc aac aac atg agg gca cca ggc cag ggg gac tac gag agg aat Asp Ala Asn Asn Met Arg Ala Pro Gly Gln Gly Asp Tyr Glu Arg Asn 580 585 590			1776
tcc gcc gat act gac ggg ctc cag gag tcg tcg cca cca atc ccc ata Ser Ala Asp Thr Asp Gly Leu Gln Glu Ser Ser Pro Pro Ile Pro Ile 595 600 605			1824
tgg aaa ccg tcg ata agc ttg cgg ccg cca ccg cgg tgg agc tcc agc Trp Lys Pro Ser Ile Ser Leu Arg Pro Pro Pro Arg Trp Ser Ser Ser 610 615 620			1872
ttt tgt tcc ctt taa Phe Cys Ser Leu 625			1887

<210> 30
 <211> 628
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AEPII 1a (clone # 63GP4)

<400> 30
 Met Ile Asn Val Ala Thr Gly Glu Glu Thr Pro Ile His Leu Phe Gly
 1 5 10 15
 Val Asn Trp Phe Gly Phe Glu Thr Pro Asn Tyr Val Val His Gly Leu
 20 25 30
 Trp Ser Arg Asn Trp Glu Asp Met Leu Leu Gln Ile Lys Ser Leu Gly
 35 40 45
 Phe Asn Ala Ile Arg Leu Pro Phe Cys Thr Gln Ser Val Lys Pro Gly
 50 55 60
 Thr Met Pro Thr Ala Ile Asp Tyr Ala Lys Asn Pro Asp Leu Gln Gly
 65 70 75 80
 Leu Asp Ser Val Gln Ile Met Glu Lys Ile Ile Lys Lys Ala Gly Asp
 85 90 95
 Leu Gly Ile Phe Val Leu Leu Asp Tyr His Arg Ile Gly Cys Asn Phe
 100 105 110
 Ile Glu Pro Leu Trp Tyr Thr Asp Ser Phe Ser Glu Gln Asp Tyr Ile
 115 120 125
 Asn Thr Trp Val Glu Val Ala Gln Arg Phe Gly Lys Tyr Trp Asn Val

130		135		140
Ile Gly Ala Asp Leu Lys Asn Glu Pro His Ser Ser Ser Pro Ala Pro				
145		150		155
Ala Ala Tyr Thr Asp Gly Ser Gly Ala Thr Trp Gly Met Gly Asn Asn				160
	165		170	175
Ala Thr Asp Trp Asn Leu Ala Ala Glu Arg Ile Gly Arg Ala Ile Leu				
	180		185	190
Glu Val Ala Pro Gln Trp Val Ile Phe Val Glu Gly Thr Gln Phe Thr				
	195	200		205
Thr Pro Glu Ile Asp Gly Arg Tyr Lys Trp Gly His Asn Ala Trp Trp				
	210	215		220
Gly Gly Asn Leu Met Gly Val Arg Lys Tyr Pro Val Asn Leu Pro Arg				
225		230		235
Asp Lys Leu Val Tyr Ser Pro Gln Val Tyr Gly Pro Asp Val Tyr Asp				240
	245		250	255
Gln Pro Tyr Phe Asp Pro Gly Glu Gly Phe Pro Asp Asn Leu Pro Glu				
	260		265	270
Ile Trp Tyr His His Phe Gly Tyr Val Lys Leu Asp Leu Gly Tyr Pro				
	275	280		285
Val Val Ile Gly Glu Phe Gly Gly Lys Tyr Gly His Gly Gly Asp Pro				
	290	295		300
Arg Asp Val Thr Trp Gln Asn Lys Ile Ile Asp Trp Met Ile Gln Asn				
305		310		315
Lys Phe Cys Asp Phe Phe Tyr Trp Ser Trp Asn Pro Asn Ser Gly Asp				
	325		330	335
Thr Gly Gly Ile Leu Lys Asp Asp Trp Thr Thr Ile Trp Glu Asp Lys				
	340		345	350
Tyr Asn Asn Leu Lys Arg Leu Met Asp Ser Cys Ser Gly Asn Ala Thr				
	355	360		365
Ala Pro Ser Val Pro Thr Thr Thr Thr Thr Thr Ser Thr Pro Pro Thr				
	370	375		380
Thr Thr Thr Thr Thr Thr Ser Thr Pro Thr Thr Thr Thr Gln Thr Pro				
385	390		395	400
Thr Thr Thr Thr Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Pro Ser				
	405		410	415
Asn Asn Val Pro Phe Glu Ile Val Asn Val Leu Pro Thr Ser Ser Gln				
	420		425	430
Tyr Glu Gly Thr Ser Val Glu Val Val Cys Asp Gly Thr Gln Cys Ala				
	435		440	445
Ser Ser Val Trp Gly Ala Pro Asn Leu Trp Gly Val Val Lys Ile Gly				
	450		455	460
Asn Ala Thr Met Asp Pro Asn Val Trp Gly Trp Glu Asp Val Tyr Lys				
465		470		475
Thr Ala Pro Gln Asp Ile Gly Thr Gly Ser Thr Lys Met Glu Ile Arg				
	485		490	495
Asn Gly Val Leu Lys Val Thr Asn Leu Trp Asn Ile Asn Met His Pro				
	500		505	510
Lys Tyr Asn Thr Met Ala Tyr Pro Glu Val Ile Tyr Gly Ala Lys Pro				
	515		520	525
Trp Gly Asn Gln Pro Ile Asn Ala Pro Asn Phe Val Leu Pro Ile Lys				
	530		535	540
Val Ser Gln Leu Pro Arg Ile Leu Val Asp Thr Lys Tyr Thr Leu Glu				
545		550		555
Lys Ser Phe Pro Gly Asn Asn Phe Ala Phe Glu Ala Trp Leu Phe Lys				
	565		570	575
Asp Ala Asn Asn Met Arg Ala Pro Gly Gln Gly Asp Tyr Glu Arg Asn				
	580		585	590
Ser Ala Asp Thr Asp Gly Leu Gln Glu Ser Ser Pro Pro Ile Pro Ile				
	595		600	605
Trp Lys Pro Ser Ile Ser Leu Arg Pro Pro Pro Arg Trp Ser Ser Ser				
	610		615	620

Phe Cys Ser Leu
625

<210> 31

<211> 1443

<212> DNA

<213> Artificial Sequence

<220>

<223> AEPII 1a (clone # 63GP4)

<221> CDS

<222> (1)...(1443)

<400> 31

gct gga gtg ggt gag caa cgg gat aac cta cca gat att ccc cga cag	48
Ala Gly Val Gly Glu Gln Arg Asp Asn Leu Pro Asp Ile Pro Arg Gln	
1 5 10 15	
ggt caa caa cgg aaa cag gag caa cga tgc cct agc ttt gga cca cga	96
Val Gln Gln Arg Lys Gln Glu Gln Arg Cys Pro Ser Phe Gly Pro Arg	
20 25 30	
cga gct aat tct gaa cca ggt caa tcc agg caa acc aat cct ctc caa	144
Arg Ala Asn Ser Glu Pro Gly Gln Ser Arg Gln Thr Asn Pro Leu Gln	
35 40 45	
ctg gag cga ccc tat aac gcc cct cca ctg ctg cca cca gta ctt cgg	192
Leu Glu Arg Pro Tyr Asn Ala Pro Pro Leu Leu Pro Pro Val Leu Arg	
50 55 60	
cgg cga cat aaa ggg aat aac gga gaa gct cga cta cct tca gag cct	240
Arg Arg His Lys Gly Asn Asn Gly Glu Ala Arg Leu Pro Ser Glu Pro	
65 70 75 80	
agg tgt tac tat aat cta cct caa ccc gat ttt cct ctc ggg aag cgc	288
Arg Cys Tyr Tyr Asn Leu Pro Gln Pro Asp Phe Pro Leu Gly Lys Arg	
85 90 95	
cca cgg cta cga cac cta cga cta cta ccg gct tga ccc caa gtt cgg	336
Pro Arg Leu Arg His Leu Arg Leu Leu Pro Ala * Pro Gln Val Arg	
100 105 110	
gac cga gga gga gct gag aga gtt cct cga tga ggc aca cag gcg ggg	384
Asp Arg Gly Gly Ala Glu Arg Val Pro Arg * Gly Thr Gln Ala Gly	
115 120 125	
aat gag ggt aat ttt cga ttt tgt gcc caa cca ctg cgg cat agg gaa	432
Asn Glu Gly Asn Phe Arg Phe Cys Ala Gln Pro Leu Arg His Arg Glu	
130 135 140	
tcc agc ctt cct aga agt ttg gaa gaa ggg caa cga aag ccc ata ctg	480
Ser Ser Leu Pro Arg Ser Leu Glu Glu Gly Gln Arg Lys Pro Ile Leu	
145 150 155	
gga ctg gtt ctt cgt caa gaa gtg gcc gtt caa gct cgg cga tgg gaa	528
Gly Leu Val Leu Arg Gln Glu Val Ala Val Gln Ala Arg Arg Trp Glu	
160 165 170	
cgc cta cgt cgg ctg gtg ggg ctt tgg gag cct tcc aaa gct caa cac	576
Arg Leu Arg Arg Leu Val Gly Leu Trp Glu Pro Ser Lys Ala Gln His	

175						180						185						190	
tgc Cys	caa Gln	ccc Pro	gga Gly	ggt Gly	cag Gln	gga Gly	ata Ile	cct Pro	gat Asp	agg Arg	agc Ser	ggc Gly	cct Pro	cca Pro	ctg Leu	624			
					195						200						205		
gat Asp	aga Arg	gtt Val	cgg Arg	ctt Leu	tga *	cgg Arg	cat His	cag Gln	ggt Gly	tga *	tgt Cys	gcc Ala	gaa Glu	cga Arg	agt Ser	672			
					210						215						220		
cct Pro	cga Arg	ccc Pro	ggg Gly	aac Asn	gtt Val	ctt Leu	ccc Pro	gga Gly	gct Ala	gag Glu	aaa Lys	ggc Gly	agt Ser	caa Gln	gga Gly	720			
					225						230						235		
gaa Glu	aaa Lys	gcc Ala	gga Gly	cgc Arg	ata Ile	cct Pro	cgt Arg	cgg Arg	tga *	gat Asp	atg Met	gac Asp	gct Ala	ctc Leu	ccc Pro	768			
					240						245						250		
tga *	gtg Val	ggt Gly	gaa Glu	agg Arg	aga Arg	ccg Pro	ctt Leu	cga Arg	ctc Leu	cct Pro	cat His	gaa Glu	cta Leu	cgc Arg	cct Pro	816			
					255						260						265		
cgg Arg	gag Glu	gga Gly	cat His	cct Pro	cct Pro	gaa Glu	cta Leu	cgc Arg	gaa Glu	ggg Gly	cct Pro	gct Ala	cag Gln	tgg Trp	aga Arg	864			
					270						275						280		
aag Lys	tgc Cys	aat Asn	gaa Glu	aat Asn	gat Asp	ggg Gly	acg Thr	tta Leu	cta Leu	tgc Cys	ttc Phe	cta Leu	cgg Arg	cga Arg	gaa Glu	912			
					285						290						295		
cgt Arg	att Ile	gcg Ala	atg Met	ggc Gly	ttc Phe	aac Asn	ctc Leu	gtt Val	gat Asp	tcg Ser	cac His	gac Asp	act Thr	tcg Ser	agg Arg	960			
					300						305						310		
<hr/>																			
gtt Val	ctc Leu	act Thr	gat Asp	ctc Leu	ggt Gly	ggg Gly	ggg Gly	agt Ser	ctc Leu	ggt Gly	gac Asp	aca Thr	ccg Pro	tca Ser	aac Asn	1008			
					315						320						325	330	
gag Glu	tca Ser	att Ile	cag Gln	aga Arg	ctc Leu	aag Lys	ctc Leu	ctc Leu	tca Ser	acg Thr	tcc Ser	tct Ser	atg Met	ccc Pro	tgc Cys	1056			
					335						340						345		
ctg Leu	gaa Glu	ctc Leu	cgg Arg	tca Ser	cct Pro	tcc Ser	agg Arg	gga Gly	tga *	gag Glu	agg Arg	act Thr	gct Ala	cgg Arg	aga Arg	1104			
					350						355						360		
caa Gln	ggg Gly	gca Ala	cta Leu	cga Arg	cga Arg	aca Thr	gcg Ala	cta Leu	ccc Pro	aat Asn	aca Thr	gtg Val	gga Gly	tac Tyr	tgt Cys	1152			
					365						370						375		
gaa Glu	cga Arg	aga Arg	cgt Arg	cct Pro	gaa Glu	cca Pro	tta Leu	cag Gln	ggc Gly	att Ile	ggc Gly	gga Gly	gct Ala	cag Gln	aaa Lys	1200			
					380						385						390		
aag Lys	agt Ser	tcc Ser	tgc Cys	att Ile	gag Glu	gag Glu	cag Gln	cgc Arg	aat Asn	aag Lys	gtt Val	cta Leu	cac His	tgc Cys	caa Gln	1248			
					395						400						405		
agg Arg	cgg Arg	cgt Arg	tat Tyr	ggc Gly	ctt Leu	ctt Leu	cag Gln	ggg Gly	gca Ala	tca Ser	tga *	cga Arg	ggt Gly	tct Ser	tgt Cys	1296			
					410						415						420		

cgt tgc caa cag ctg gaa gaa gcc agc cct act aaa gct tcc tga ggg 1344
 Arg Cys Gln Gln Leu Glu Glu Ala Ser Pro Thr Lys Ala Ser * Gly
 425 430 435

aga gtg gaa agt aat ctg gcc tga gaa ttt cag ccc gga act gct tcg 1392
 Arg Val Glu Ser Asn Leu Ala * Glu Phe Gln Pro Gly Thr Ala Ser
 440 445 450

cgg caa agt tga agt gcc agc cat agg gat aat cat cct tga gcg gag 1440
 Arg Gln Ser * Ser Ala Ser His Arg Asp Asn His Pro * Ala Glu
 455 460 465

ttg 1443
 Leu

<210> 32

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> AEPII 1a (clone # 63GP4)

<400> 32

Ala Gly Val Gly Glu Gln Arg Asp Asn Leu Pro Asp Ile Pro Arg Gln
 1 5 10 15
 Val Gln Gln Arg Lys Gln Glu Gln Arg Cys Pro Ser Phe Gly Pro Arg
 20 25 30
 Arg Ala Asn Ser Glu Pro Gly Gln Ser Arg Gln Thr Asn Pro Leu Gln
 35 40 45

Leu Glu Arg Pro Tyr Asn Ala Pro Pro Leu Leu Pro Pro Val Leu Arg
 50 55 60
 Arg Arg His Lys Gly Asn Asn Gly Glu Ala Arg Leu Pro Ser Glu Pro
 65 70 75 80
 Arg Cys Tyr Tyr Asn Leu Pro Gln Pro Asp Phe Pro Leu Gly Lys Arg
 85 90 95
 Pro Arg Leu Arg His Leu Arg Leu Leu Pro Ala Pro Gln Val Arg Asp
 100 105 110
 Arg Gly Gly Ala Glu Arg Val Pro Arg Gly Thr Gln Ala Gly Asn Glu
 115 120 125
 Gly Asn Phe Arg Phe Cys Ala Gln Pro Leu Arg His Arg Glu Ser Ser
 130 135 140
 Leu Pro Arg Ser Leu Glu Gly Gln Arg Lys Pro Ile Leu Gly Leu
 145 150 155 160
 Val Leu Arg Gln Glu Val Ala Val Gln Ala Arg Arg Trp Glu Arg Leu
 165 170 175
 Arg Arg Leu Val Gly Leu Trp Glu Pro Ser Lys Ala Gln His Cys Gln
 180 185 190
 Pro Gly Gly Gln Gly Ile Pro Asp Arg Ser Gly Pro Pro Leu Asp Arg
 195 200 205
 Val Arg Leu Arg His Gln Gly Cys Ala Glu Arg Ser Pro Arg Pro Gly
 210 215 220
 Asn Val Leu Pro Gly Ala Glu Lys Gly Ser Gln Gly Glu Lys Ala Gly
 225 230 235 240
 Arg Ile Pro Arg Arg Asp Met Asp Ala Leu Pro Val Gly Glu Arg Arg
 245 250 255
 Pro Leu Arg Leu Pro His Glu Leu Arg Pro Arg Glu Gly His Pro Pro
 260 265 270

[illegible]

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<210> 33
<211> 1032
<212> DNA
<213> Bacillus thermoloeovorans
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<220> -----
<221> CDS
<222> (1)...(1032)
<223> clone # 68GC1
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<400> 33																
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Met	Thr	Glu	Leu	Tyr	Ile	Lys	Asn	Pro	Leu	Ile	Glu	Gln	Arg	Ala	Asp	
1		5				10				15						
ccc	tgg	atc	tat	aaa	cat	acc	gat	ggt	tat	tat	tac	ttt	acc	ggt	tcc	96
Pro	Trp	Ile	Tyr	Lys	His	Thr	Asp	Gly	Tyr	Tyr	Tyr	Phe	Thr	Gly	Ser	
			20		25				30							
gtg	ccg	gag	tac	gac	cga	att	gag	ctt	aga	cgc	tcg	caa	acg	att	caa	144
Val	Pro	Glu	Tyr	Asp	Arg	Ile	Glu	Leu	Arg	Arg	Ser	Gln	Thr	Ile	Gln	
35		40				45										
ggg	ctt	gcg	gat	gcc	gaa	gga	att	acg	atc	tgg	cgc	aag	cat	gag	tca	192
Gly	Leu	Ala	Asp	Ala	Glu	Gly	Ile	Thr	Ile	Trp	Arg	Lys	His	Glu	Ser	
50		55				60										
ggc	ctg	atg	agt	gcc	aac	ata	tgg	gca	ccc	gag	att	cat	tat	atg	gat	240
Gly	Leu	Met	Ser	Ala	Asn	Ile	Trp	Ala	Pro	Glu	Ile	His	Tyr	Met	Asp	
65		70				75				80						
ggc	aaa	tgg	tat	gtg	tat	tac	gcc	gct	gcc	cat	act	tca	gaa	acg	agg	288
Gly	Lys	Trp	Tyr	Val	Tyr	Tyr	Ala	Ala	Ala	His	Thr	Ser	Glu	Thr	Arg	
			85		90				95							

gac gga ttg ttc gat cac cgc atg ttc gta ttg gag aac gct tcg gcg Asp Gly Leu Phe Asp His Arg Met Phe Val Leu Glu Asn Ala Ser Ala 100 105 110	336
aac ccg ctc gaa ggg gaa tgg gtg gag aag ggg caa gtg atc acg aag Asn Pro Leu Glu Gly Glu Trp Val Glu Lys Gly Gln Val Ile Thr Lys 115 120 125	384
tgg gaa tct ttc gcc ttg gac gca acg acg ttc gag cat aaa ggc aaa Trp Glu Ser Phe Ala Leu Asp Ala Thr Thr Phe Glu His Lys Gly Lys 130 135 140	432
cgg tac tat gta tgg gct cag aaa gat ccg ggc att cca ggc aat tcc Arg Tyr Tyr Val Trp Ala Gln Lys Asp Pro Gly Ile Pro Gly Asn Ser 145 150 155 160	480
aat ctg tat atc tca ttg atg gaa gac ccg tgg acc ctg aca ggg gaa Asn Leu Tyr Ile Ser Leu Met Glu Asp Pro Trp Thr Leu Thr Gly Glu 165 170 175	528
cag gta tgc ata tcg gtt ccc gag tac gat tgg gag aag atc ggg tat Gln Val Cys Ile Ser Val Pro Glu Tyr Asp Trp Glu Lys Ile Gly Tyr 180 185 190	576
ctt gtg aat gaa ggg gcc gcc gtt ctt aag cga aac ggg cga ata ttc Leu Val Asn Glu Gly Ala Ala Val Leu Lys Arg Asn Gly Arg Ile Phe 195 200 205	624
atg acc tat tcc gcg agc gcc acg gac cac aac tat gcg atg ggg ctg Met Thr Tyr Ser Ala Ser Ala Thr Asp His Asn Tyr Ala Met Gly Leu 210 215 220	672
ctg aca gcc gat gaa gac agt gat ttg ctg aat ccg agc tcc tgg gtc Leu Thr Ala Asp Glu Asp Ser Asp Leu Leu Asn Pro Ser Ser Trp Val 225 230 235 240	720
aag tcg cct gta cct gta ttt acg aca tct gaa gcc aat ggc caa tat Lys Ser Pro Val Pro Val Phe Thr Thr Ser Glu Ala Asn Gly Gln Tyr 245 250 255	768
ggt ccg ggg cac aac agc ttc acg att tcc gag gac ggc ttg cag gac Gly Pro Gly His Asn Ser Phe Thr Ile Ser Glu Asp Gly Leu Gln Asp 260 265 270	816
att ttg gta tac cat gca aga agt tac aag gag atc gtc ggg atc cac Ile Leu Val Tyr His Ala Arg Ser Tyr Lys Glu Ile Val Gly Ile His 275 280 285	864
tat atg atc cga acc gtc ata cgc gtg tac agg tca tcc gat gga acg Tyr Met Ile Arg Thr Val Ile Arg Val Tyr Arg Ser Ser Asp Gly Thr 290 295 300	912
aag acg gaa cgc cga att tcg ggg tgc caa gag cgg atc atg aac cgg Lys Thr Glu Arg Arg Ile Ser Gly Cys Gln Glu Arg Ile Met Asn Arg 305 310 315 320	960
tct cca agc cat gat gcc gac ttt gtc att ggg gtt gtg acc gga agg Ser Pro Ser His Asp Ala Asp Phe Val Ile Gly Val Val Thr Gly Arg 325 330 335	1008

att aac aaa cat cag acc gac tga
 Ile Asn Lys His Gln Thr Asp *
 340

1032

<210> 34
 <211> 343
 <212> PRT
 <213> *Bacillus thermoloeovorans*

<400> 34
 Met Thr Glu Leu Tyr Ile Lys Asn Pro Leu Ile Glu Gln Arg Ala Asp
 1 5 10 15
 Pro Trp Ile Tyr Lys His Thr Asp Gly Tyr Tyr Tyr Phe Thr Gly Ser
 20 25 30
 Val Pro Glu Tyr Asp Arg Ile Glu Leu Arg Arg Ser Gln Thr Ile Gln
 35 40 45
 Gly Leu Ala Asp Ala Glu Gly Ile Thr Ile Trp Arg Lys His Glu Ser
 50 55 60
 Gly Leu Met Ser Ala Asn Ile Trp Ala Pro Glu Ile His Tyr Met Asp
 65 70 75 80
 Gly Lys Trp Tyr Val Tyr Tyr Ala Ala Ala His Thr Ser Glu Thr Arg
 85 90 95
 Asp Gly Leu Phe Asp His Arg Met Phe Val Leu Glu Asn Ala Ser Ala
 100 105 110
 Asn Pro Leu Glu Gly Glu Trp Val Glu Lys Gly Gln Val Ile Thr Lys
 115 120 125
 Trp Glu Ser Phe Ala Leu Asp Ala Thr Thr Phe Glu His Lys Gly Lys
 130 135 140
 Arg Tyr Tyr Val Trp Ala Gln Lys Asp Pro Gly Ile Pro Gly Asn Ser
 145 150 155 160
 Asn Leu Tyr Ile Ser Leu Met Glu Asp Pro Trp Thr Leu Thr Gly Glu
 165 170 175
 Gln Val Cys Ile Ser Val Pro Glu Tyr Asp Trp Glu Lys Ile Gly Tyr
 180 185 190
 Leu Val Asn Glu Gly Ala Ala Val Leu Lys Arg Asn Gly Arg Ile Phe
 195 200 205
 Met Thr Tyr Ser Ala Ser Ala Thr Asp His Asn Tyr Ala Met Gly Leu
 210 215 220
 Leu Thr Ala Asp Glu Asp Ser Asp Leu Leu Asn Pro Ser Ser Trp Val
 225 230 235 240
 Lys Ser Pro Val Pro Val Phe Thr Thr Ser Glu Ala Asn Gly Gln Tyr
 245 250 255
 Gly Pro Gly His Asn Ser Phe Thr Ile Ser Glu Asp Gly Leu Gln Asp
 260 265 270
 Ile Leu Val Tyr His Ala Arg Ser Tyr Lys Glu Ile Val Gly Ile His
 275 280 285
 Tyr Met Ile Arg Thr Val Ile Arg Val Tyr Arg Ser Ser Asp Gly Thr
 290 295 300
 Lys Thr Glu Arg Arg Ile Ser Gly Cys Gln Glu Arg Ile Met Asn Arg
 305 310 315 320
 Ser Pro Ser His Asp Ala Asp Phe Val Ile Gly Val Val Thr Gly Arg
 325 330 335
 Ile Asn Lys His Gln Thr Asp
 340

<210> 35
 <211> 990
 <212> DNA
 <213> *Thermotoga maritima*

<220>

<221> CDS

<222> (1)...(990)

<400> 35

ttg	aat	aac	acc	att	cca	aga	tgg	cgt	ggt	ttc	aac	ctt	ctg	gag	gcc	48
Leu	Asn	Asn	Thr	Ile	Pro	Arg	Trp	Arg	Gly	Phe	Asn	Leu	Leu	Glu	Ala	
1				5				10					15			

ttt	tcc	att	aaa	agt	aca	gga	aat	ttt	aaa	gag	gaa	gat	ttt	ttg	tgg	96
Phe	Ser	Ile	Lys	Ser	Thr	Gly	Asn	Phe	Lys	Glu	Glu	Asp	Phe	Leu	Trp	
			20				25						30			

atg	gct	cag	tgg	gac	ttt	aat	ttt	gtt	aga	atc	cct	atg	tgt	cat	ctt	144
Met	Ala	Gln	Trp	Asp	Phe	Asn	Phe	Val	Arg	Ile	Pro	Met	Cys	His	Leu	
		35					40					45				

ctc	tgg	tca	gac	cgg	ggc	aac	cca	ttt	att	atc	aga	gaa	gat	ttt	ttt	192
Leu	Trp	Ser	Asp	Arg	Gly	Asn	Pro	Phe	Ile	Ile	Arg	Glu	Asp	Phe	Phe	
	50					55					60					

gag	aaa	atc	gat	cgt	gta	att	ttc	tgg	gga	gag	aaa	tat	gga	ata	cat	240
Glu	Lys	Ile	Asp	Arg	Val	Ile	Phe	Trp	Gly	Glu	Lys	Tyr	Gly	Ile	His	
65					70				75					80		

ata	tgt	att	tct	ctt	cac	agg	gca	cct	ggc	tat	tct	gtt	aac	aag	gaa	288
Ile	Cys	Ile	Ser	Leu	His	Arg	Ala	Pro	Gly	Tyr	Ser	Val	Asn	Lys	Glu	
				85				90					95			

gta	gaa	gag	aaa	acc	aat	ctg	tgg	aaa	gat	gaa	aca	gct	caa	gaa	gcg	336
Val	Glu	Glu	Lys	Thr	Asn	Leu	Trp	Lys	Asp	Glu	Thr	Ala	Gln	Glu	Ala	
			100				105						110			

ttc	att	cat	cac	tgg	tct	ttt	atc	gca	cgt	cgt	tac	aaa	gga	att	tct	384
Phe	Ile	His	His	Trp	Ser	Phe	Ile	Ala	Arg	Arg	Tyr	Lys	Gly	Ile	Ser	
		115					120					125				

tcc	aca	cac	ctg	agt	ttt	aac	tta	ata	aat	gag	cct	cca	ttt	cct	gat	432
Ser	Thr	His	Leu	Ser	Phe	Asn	Leu	Ile	Asn	Glu	Pro	Pro	Phe	Pro	Asp	
	130					135					140					

cca	caa	atc	atg	agt	gtt	gaa	gat	cac	aac	tct	ctt	atc	aag	aga	act	480
Pro	Gln	Ile	Met	Ser	Val	Glu	Asp	His	Asn	Ser	Leu	Ile	Lys	Arg	Thr	
145					150					155				160		

att	aca	gaa	att	cga	aaa	ata	gat	ccc	gaa	aga	tta	att	ata	ata	gat	528
Ile	Thr	Glu	Ile	Arg	Lys	Ile	Asp	Pro	Glu	Arg	Leu	Ile	Ile	Ile	Asp	
				165				170					175			

gga	tta	ggc	tat	ggg	aat	att	cca	gtg	gat	gat	tta	aca	att	gag	aat	576
Gly	Leu	Gly	Tyr	Gly	Asn	Ile	Pro	Val	Asp	Asp	Leu	Thr	Ile	Glu	Asn	
		180						185					190			

aca	gtg	caa	tca	tgc	aga	ggg	tac	att	ccc	ttc	agt	gtt	act	cat	tac	624
Thr	Val	Gln	Ser	Cys	Arg	Gly	Tyr	Ile	Pro	Phe	Ser	Val	Thr	His	Tyr	
		195				200						205				

aaa	gcg	gaa	tgg	gtg	gat	agt	aag	gac	ttt	cct	gtt	cct	gag	tgg	cca	672
Lys	Ala	Glu	Trp	Val	Asp	Ser	Lys	Asp	Phe	Pro	Val	Pro	Glu	Trp	Pro	
	210					215					220					

aat gga tgg cat ttt ggg gaa tac tgg aac aga gaa aag tta ttg gaa 720
 Asn Gly Trp His Phe Gly Glu Tyr Trp Asn Arg Glu Lys Leu Leu Glu
 225 230 235 240
 cat tat tta acg tgg ata aaa ctc aga caa aaa gga ata gaa gta ttc 768
 His Tyr Leu Thr Trp Ile Lys Leu Arg Gln Lys Gly Ile Glu Val Phe
 245 250 255
 tgt gga gaa atg gga gct tac aac aaa aca cct cac gat gtg gtt tta 816
 Cys Gly Glu Met Gly Ala Tyr Asn Lys Thr Pro His Asp Val Val Leu
 260 265 270
 aaa tgg ctt gaa gat ctt tta gaa att ttt aaa act ttg aac ata ggg 864
 Lys Trp Leu Glu Asp Leu Leu Glu Ile Phe Lys Thr Leu Asn Ile Gly
 275 280 285
 ttt gcc tta tgg aat ttt aga ggt cct ttt ggt att tta gat tcg gaa 912
 Phe Ala Leu Trp Asn Phe Arg Gly Pro Phe Gly Ile Leu Asp Ser Glu
 290 295 300
 agg aaa gac gtt gaa tac gaa gaa tgg tat gga cat aaa ctg gat agg 960
 Arg Lys Asp Val Glu Tyr Glu Glu Trp Tyr Gly His Lys Leu Asp Arg
 305 310 315 320
 aaa atg ttg gaa cta ttg aga aaa tat tag 990
 Lys Met Leu Glu Leu Leu Arg Lys Tyr *
 325

<210> 36

<211> 329

<212> PRT

<213> *Thermotoga maritima*

<400> 36

Leu Asn Asn Thr Ile Pro Arg Trp Arg Gly Phe Asn Leu Leu Glu Ala
 1 5 10 15
 Phe Ser Ile Lys Ser Thr Gly Asn Phe Lys Glu Glu Asp Phe Leu Trp
 20 25 30
 Met Ala Gln Trp Asp Phe Asn Phe Val Arg Ile Pro Met Cys His Leu
 35 40 45
 Leu Trp Ser Asp Arg Gly Asn Pro Phe Ile Ile Arg Glu Asp Phe Phe
 50 55 60
 Glu Lys Ile Asp Arg Val Ile Phe Trp Gly Glu Lys Tyr Gly Ile His
 65 70 75 80
 Ile Cys Ile Ser Leu His Arg Ala Pro Gly Tyr Ser Val Asn Lys Glu
 85 90 95
 Val Glu Glu Lys Thr Asn Leu Trp Lys Asp Glu Thr Ala Gln Glu Ala
 100 105 110
 Phe Ile His His Trp Ser Phe Ile Ala Arg Arg Tyr Lys Gly Ile Ser
 115 120 125
 Ser Thr His Leu Ser Phe Asn Leu Ile Asn Glu Pro Pro Phe Pro Asp
 130 135 140
 Pro Gln Ile Met Ser Val Glu Asp His Asn Ser Leu Ile Lys Arg Thr
 145 150 155 160
 Ile Thr Glu Ile Arg Lys Ile Asp Pro Glu Arg Leu Ile Ile Ile Asp
 165 170 175
 Gly Leu Gly Tyr Gly Asn Ile Pro Val Asp Asp Leu Thr Ile Glu Asn
 180 185 190
 Thr Val Gln Ser Cys Arg Gly Tyr Ile Pro Phe Ser Val Thr His Tyr
 195 200 205

Lys Ala Glu Trp Val Asp Ser Lys Asp Phe Pro Val Pro Glu Trp Pro
 210 215 220
 Asn Gly Trp His Phe Gly Glu Tyr Trp Asn Arg Glu Lys Leu Leu Glu
 225 230 235 240
 His Tyr Leu Thr Trp Ile Lys Leu Arg Gln Lys Gly Ile Glu Val Phe
 245 250 255
 Cys Gly Glu Met Gly Ala Tyr Asn Lys Thr Pro His Asp Val Val Leu
 260 265 270
 Lys Trp Leu Glu Asp Leu Leu Glu Ile Phe Lys Thr Leu Asn Ile Gly
 275 280 285
 Phe Ala Leu Trp Asn Phe Arg Gly Pro Phe Gly Ile Leu Asp Ser Glu
 290 295 300
 Arg Lys Asp Val Glu Tyr Glu Glu Trp Tyr Gly His Lys Leu Asp Arg
 305 310 315 320
 Lys Met Leu Glu Leu Leu Arg Lys Tyr
 325

<210> 37
 <211> 3012
 <212> DNA
 <213> Thermotoga maritima

<220>
 <221> CDS
 <222> (1)...(3012)
 <223> clone # 6GC17

<400> 37
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 Met Leu Ser Glu Ile Val Pro Tyr Thr Val Leu Arg Arg Glu Arg Ile
 1 5 10 15

 gaa agc tgg att ttc tcc gat gat gct gtt gag aga atc gtg gat cct 96
 Glu Ser Trp Ile Phe Ser Asp Asp Ala Val Glu Arg Ile Val Asp Pro
 20 25 30
 tcc ttc gaa tgg gac ttc agc tcc gct ccc gtc cgg ttc agg aaa gag 144
 Ser Phe Glu Trp Asp Phe Ser Ser Ala Pro Val Arg Phe Arg Lys Glu
 35 40 45
 cta gag cct ttc tcc gtc gct gga gag cag agg gcc tac ctg aaa ctc 192
 Leu Glu Pro Phe Ser Val Ala Gly Glu Gln Arg Ala Tyr Leu Lys Leu
 50 55 60
 tgg ttc ggt ggt gaa aca ctc gtt ctg ata gat ggg aag cct tac ggt 240
 Trp Phe Gly Gly Glu Thr Leu Val Leu Ile Asp Gly Lys Pro Tyr Gly
 65 70 75 80
 gag atc aac gag tat cat agg atg ttg aac atc acc ccc ctt gct gat 288
 Glu Ile Asn Glu Tyr His Arg Met Leu Asn Ile Thr Pro Leu Ala Asp
 85 90 95
 gga aaa cca cac acg ata gaa gct cag gtg atg cca agg ggt ctc ttt 336
 Gly Lys Pro His Thr Ile Glu Ala Gln Val Met Pro Arg Gly Leu Phe
 100 105 110
 gga aaa cca gaa aag ccg gtg ttc acg gaa gct ttc ttc atc gtc gtt 384
 Gly Lys Pro Glu Lys Pro Val Phe Thr Glu Ala Phe Phe Ile Val Val
 115 120 125
 gat gaa gca ctg atg aag gtg gtg aaa act ctc gaa ctc act ata aaa 432

Asp	Glu	Ala	Leu	Met	Lys	Val	Val	Lys	Thr	Leu	Glu	Leu	Thr	Ile	Lys	
130						135					140					
acg	gca	gaa	gtg	ata	gaa	gac	gag	tcg	ctt	tct	aag	aaa	ctt	ctg	gac	480
Thr	Ala	Glu	Val	Ile	Glu	Asp	Glu	Ser	Leu	Ser	Lys	Lys	Leu	Leu	Asp	
145					150				155						160	
atc	tcc	gag	gag	ttt	ctc	tcg	aaa	gta	tgg	atc	cca	aga	gac	aca	ggc	528
Ile	Ser	Glu	Glu	Phe	Leu	Ser	Lys	Val	Trp	Ile	Pro	Arg	Asp	Thr	Gly	
				165				170						175		
acc	tat	ctg	atg	aca	gca	ctg	gag	gat	ccg	gga	ata	aaa	gat	gag	atc	576
Thr	Tyr	Leu	Met	Thr	Ala	Leu	Glu	Asp	Pro	Gly	Ile	Lys	Asp	Glu	Ile	
			180					185					190			
aaa	aac	acc	tgg	aac	aca	ccg	gag	ttc	aaa	gag	ttc	aca	ggc	gtg	aag	624
Lys	Asn	Thr	Trp	Asn	Thr	Pro	Glu	Phe	Lys	Glu	Phe	Thr	Gly	Val	Lys	
		195					200					205				
ctt	cct	gaa	gag	ttg	aga	aat	cag	att	ctg	gaa	gag	ttc	gaa	aaa	ttc	672
Leu	Pro	Glu	Glu	Leu	Arg	Asn	Gln	Ile	Leu	Glu	Glu	Phe	Glu	Lys	Phe	
	210					215						220				
aaa	gaa	aag	ctg	gat	aga	ata	aga	aaa	aac	cat	ccg	ggc	ttt	gga	acg	720
Lys	Glu	Lys	Leu	Asp	Arg	Ile	Arg	Lys	Asn	His	Pro	Gly	Phe	Gly	Thr	
225					230					235					240	
att	cac	ctt	gtg	ggg	cac	gcg	cac	ata	gac	tac	gcc	tgg	ctc	tgg	cca	768
Ile	His	Leu	Val	Gly	His	Ala	His	Ile	Asp	Tyr	Ala	Trp	Leu	Trp	Pro	
				245					250					255		
gtt	gag	gag	acg	aag	aga	aag	atc	cta	cgc	act	ttc	gca	aac	tct	gtg	816
Val	Glu	Glu	Thr	Lys	Arg	Lys	Ile	Leu	Arg	Thr	Phe	Ala	Asn	Ser	Val	
			260					265					270			
ttg	ctc	tct	aag	ctt	tat	ccg	gag	ttc	gtt	tac	act	cag	tct	tct	gct	864
Leu	Leu	Ser	Lys	Leu	Tyr	Pro	Glu	Phe	Val	Tyr	Thr	Gln	Ser	Ser	Ala	
		275					280					285				
cag	atg	tac	gag	gat	ctc	aag	caa	aat	tca	cca	gag	ctt	ttc	gag	gaa	912
Gln	Met	Tyr	Glu	Asp	Leu	Lys	Gln	Asn	Ser	Pro	Glu	Leu	Phe	Glu	Glu	
	290					295					300					
gtg	aga	aag	ctc	gta	gaa	gag	ggg	aga	tgg	gag	cca	gtc	ggc	ggc	atg	960
Val	Arg	Lys	Leu	Val	Glu	Glu	Gly	Arg	Trp	Glu	Pro	Val	Gly	Gly	Met	
305					310					315					320	
tgg	gtg	gag	tcg	gac	tgc	aac	gtt	cca	tcg	ata	gag	tcg	ctt	gtg	aga	1008
Trp	Val	Glu	Ser	Asp	Cys	Asn	Val	Pro	Ser	Ile	Glu	Ser	Leu	Val	Arg	
				325					330					335		
cag	ttc	tac	tat	ggg	caa	aaa	ttc	ttc	gaa	aga	gaa	ttc	ggg	aaa	aag	1056
Gln	Phe	Tyr	Tyr	Gly	Gln	Lys	Phe	Phe	Glu	Arg	Glu	Phe	Gly	Lys	Lys	
			340					345					350			
agc	aag	gtg	tgc	tgg	ctt	ccg	gat	gtg	ttt	ggg	ttt	tcc	tgg	gtg	ctt	1104
Ser	Lys	Val	Cys	Trp	Leu	Pro	Asp	Val	Phe	Gly	Phe	Ser	Trp	Val	Leu	
		355					360					365				
ccc	caa	att	ctg	aaa	gaa	gcc	ggg	ata	aaa	tac	ttc	gtc	acc	acg	aaa	1152
Pro	Gln	Ile	Leu	Lys	Glu	Ala	Gly	Ile	Lys	Tyr	Phe	Val	Thr	Thr	Lys	

370	375	380	
ctc aac tgg aac gac acg aac gag ttt ccg tac gat ctg tgc cgc tgg Leu Asn Trp Asn Asp Thr Asn Glu Phe Pro Tyr Asp Leu Cys Arg Trp 385 390 395 400			1200
agg gga ata gat gga tcc gaa gtg atc tat ttc agt ttc aaa aat ccc Arg Gly Ile Asp Gly Ser Glu Val Ile Tyr Phe Ser Phe Lys Asn Pro 405 410 415			1248
aac gag ggg tac aac gga aag ata gat ccc gat acg gtc tac aaa acc Asn Glu Gly Tyr Asn Gly Lys Ile Asp Pro Asp Thr Val Tyr Lys Thr 420 425 430			1296
tgg aag aac ttc agg cag aaa gat ctc aca aac aga gtt ctt ctt tcg Trp Lys Asn Phe Arg Gln Lys Asp Leu Thr Asn Arg Val Leu Leu Ser 435 440 445			1344
ttc gga cac ggt gat ggt ggt ggc ggt cca acc gaa gag atg ctg gaa Phe Gly His Gly Asp Gly Gly Gly Pro Thr Glu Glu Met Leu Glu 450 455 460			1392
aat tac gag gtt ctg aag gat ttc cct gga cta ccg cac ctt gaa atg Asn Tyr Glu Val Leu Lys Asp Phe Pro Gly Leu Pro His Leu Glu Met 465 470 475 480			1440
gga act gtg gaa gaa ttt ttc aag aag gtg gag atc gac gaa gaa ctc Gly Thr Val Glu Glu Phe Phe Lys Lys Val Glu Ile Asp Glu Glu Leu 485 490 495			1488
cct gtg tgg gac gga gag ctt tac ctt gaa ctt cac agg gga acc tac Pro Val Trp Asp Gly Glu Leu Tyr Leu Glu Leu His Arg Gly Thr Tyr 500 505 510			1536
act tct cag ttc agg aca aag aaa ctt cac aaa gaa gcg gaa gac agt Thr Ser Gln Phe Arg Thr Lys Lys Leu His Lys Glu Ala Glu Asp Ser 515 520 525			1584
ctt tat ctt gca gag ttg atc tcg gct ttc acg gat aaa gat ttt tcg Leu Tyr Leu Ala Glu Leu Ile Ser Ala Phe Thr Asp Lys Asp Phe Ser 530 535 540			1632
gac gaa ata gac gaa ctc tgg aag att ctg ttg aga aac gaa ttt cac Asp Glu Ile Asp Glu Leu Trp Lys Ile Leu Leu Arg Asn Glu Phe His 545 550 555 560			1680
gat att cta cct gga tct tct ata aag gaa gtc tat gaa gat aca gaa Asp Ile Leu Pro Gly Ser Ser Ile Lys Glu Val Tyr Glu Asp Thr Glu 565 570 575			1728
aaa gag ctc aga cat gtg ata gaa aaa tca aaa gac atc gtt atc gaa Lys Glu Leu Arg His Val Ile Glu Lys Ser Lys Asp Ile Val Ile Glu 580 585 590			1776
tct ctc aaa gtt ctt tcc tct gag aac aaa gat gtt cta acc att ttg Ser Leu Lys Val Leu Ser Ser Glu Asn Lys Asp Val Leu Thr Ile Leu 595 600 605			1824
aac gct tca tcg ttt cca aag aag tgt ctt ttc ttc ctc aac gaa gat Asn Ala Ser Ser Phe Pro Lys Lys Cys Leu Phe Phe Leu Asn Glu Asp 610 615 620			1872

ctc gcg att tcc ttt gaa gga gaa gca ctc ttg aaa cag aaa act cac Leu Ala Ile Ser Phe Glu Gly Glu Ala Leu Leu Lys Gln Lys Thr His 625 630 635 640	1920
gat gga agg tat gtg tac ttc ata gac agg gag att cct ccg ttc acg Asp Gly Arg Tyr Val Tyr Phe Ile Asp Arg Glu Ile Pro Pro Phe Thr 645 650 655	1968
aaa gta gaa ctg aaa gtt cgc aaa gcc acg tct gag gaa act cca agt Lys Val Glu Leu Lys Val Arg Lys Ala Thr Ser Glu Glu Thr Pro Ser 660 665 670	2016
gag ttg aga gaa aca aac atc atg gag aac gaa ttt ctc agg gtg cac Glu Leu Arg Glu Thr Asn Ile Met Glu Asn Glu Phe Leu Arg Val His 675 680 685	2064
gtc aac gat gac gga aca att caa atc tac gac aaa gaa ctg gac agg Val Asn Asp Asp Gly Thr Ile Gln Ile Tyr Asp Lys Glu Leu Asp Arg 690 695 700	2112
tac gtt ttc gaa gag aag gga aac atc ttg aaa ctt cat aaa aac atc Tyr Val Phe Glu Glu Lys Gly Asn Ile Leu Lys Leu His Lys Asn Ile 705 710 715 720	2160
cct gct tac tgg gac aac tgg gat atc gca gaa aac gtg gaa aag aca Pro Ala Tyr Trp Asp Asn Trp Asp Ile Ala Glu Asn Val Glu Lys Thr 725 730 735	2208
gga tat acc ctg agg gcg aaa aac ata gaa aaa ata gag tct ggc cct Gly Tyr Thr Leu Arg Ala Lys Asn Ile Glu Lys Ile Glu Ser Gly Pro 740 745 750	2256
gtt cga gaa gtg atc cgt gtt gaa cat gaa tca gaa gga agc agg atc Val Arg Glu Val Ile Arg Val Glu His Glu Ser Glu Gly Ser Arg Ile 755 760 765	2304
acg cag cat tac atc ctt tac aga aag agt aga agg ctc gat ata gaa Thr Gln His Tyr Ile Leu Tyr Arg Lys Ser Arg Arg Leu Asp Ile Glu 770 775 780	2352
acg aag gta gac tgg cac aca agg cgt gcg ctt ctc aga gcc tac ttc Thr Lys Val Asp Trp His Thr Arg Arg Ala Leu Leu Arg Ala Tyr Phe 785 790 795 800	2400
cca aca act gtt ctg tcg aga aag gct agg ttc gat atc tcc ggt ggt Pro Thr Thr Val Leu Ser Arg Lys Ala Arg Phe Asp Ile Ser Gly Gly 805 810 815	2448
ttc atc gaa agg ccc aca cac aga aac acc agt ttc gaa cag gcg cgt Phe Ile Glu Arg Pro Thr His Arg Asn Thr Ser Phe Glu Gln Ala Arg 820 825 830	2496
ttc gag gtg ccg ttt cac agg tgg atg gat ctt tcc cag aca gac ttc Phe Glu Val Pro Phe His Arg Trp Met Asp Leu Ser Gln Thr Asp Phe 835 840 845	2544
ggc gtg tcc att ctg aac gac gga aaa tac ggt ggc agt gtt cat cag Gly Val Ser Ile Leu Asn Asp Gly Lys Tyr Gly Gly Ser Val His Gln 850 855 860	2592

ggt atc atg gcg ctt tca ctg ata aaa gcg ggt att ttc ccc gat ttt 2640
 Gly Ile Met Ala Leu Ser Leu Ile Lys Ala Gly Ile Phe Pro Asp Phe
 865 870 875 880
 ctc tgt gac gaa ggc gaa cac act ttc acc tat tct gtc tac gta cac 2688
 Leu Cys Asp Glu Gly Glu His Thr Phe Thr Tyr Ser Val Tyr Val His
 885 890 895
 cct gga gac agc ttg aga gat gtt gta aaa gga tca gaa gat ctc aac 2736
 Pro Gly Asp Ser Leu Arg Asp Val Val Lys Gly Ser Glu Asp Leu Asn
 900 905 910
 aga tct ttc atc gtt cat cgc ggg gtg ttg aac ctc ccc tct cct tta 2784
 Arg Ser Phe Ile Val His Arg Gly Val Leu Asn Leu Pro Ser Pro Leu
 915 920 925
 ctg gag atc tct cct caa aac ttc cgt ctc acc tca ctg aga agg gtg 2832
 Leu Glu Ile Ser Pro Gln Asn Phe Arg Leu Thr Ser Leu Arg Arg Val
 930 935 940
 aag gac aaa att gtt ttg agg ctt gtt gag att ttc gga aca tca ggg 2880
 Lys Asp Lys Ile Val Leu Arg Leu Val Glu Ile Phe Gly Thr Ser Gly
 945 950 955 960
 aaa ctt tcc att aaa ctc cca tgg cat ggt gaa atc tat cag acg aac 2928
 Lys Leu Ser Ile Lys Leu Pro Trp His Gly Glu Ile Tyr Gln Thr Asn
 965 970 975
 gtt ctg gaa gag aaa aaa cag aaa gtc acc ttc cca gtg gtt tac cat 2976
 Val Leu Glu Glu Lys Lys Gln Lys Val Thr Phe Pro Val Val Tyr His
 980 985 990
 ccg ttc aag atc tac act ttt gtt gta gaa ggt tga 3012
 Pro Phe Lys Ile Tyr Thr Phe Val Val Glu Gly *
 995 1000

<210> 38
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 <212> PRT
 <213> Thermotoga maritima

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 Ser Phe Glu Trp Asp Phe Ser Ser Ala Pro Val Arg Phe Arg Lys Glu
 35 40 45
 Leu Glu Pro Phe Ser Val Ala Gly Glu Gln Arg Ala Tyr Leu Lys Leu
 50 55 60
 Trp Phe Gly Gly Glu Thr Leu Val Leu Ile Asp Gly Lys Pro Tyr Gly
 65 70 75 80
 Glu Ile Asn Glu Tyr His Arg Met Leu Asn Ile Thr Pro Leu Ala Asp
 85 90 95
 Gly Lys Pro His Thr Ile Glu Ala Gln Val Met Pro Arg Gly Leu Phe
 100 105 110
 Gly Lys Pro Glu Lys Pro Val Phe Thr Glu Ala Phe Phe Ile Val Val
 115 120 125
 Asp Glu Ala Leu Met Lys Val Val Lys Thr Leu Glu Leu Thr Ile Lys
 130 135 140

Thr	Ala	Glu	Val	Ile	Glu	Asp	Glu	Ser	Leu	Ser	Lys	Lys	Leu	Leu	Asp	145	150	155	160
Ile	Ser	Glu	Glu	Phe	Leu	Ser	Lys	Val	Trp	Ile	Pro	Arg	Asp	Thr	Gly	165	170		175
Thr	Tyr	Leu	Met	Thr	Ala	Leu	Glu	Asp	Pro	Gly	Ile	Lys	Asp	Glu	Ile	180	185		190
Lys	Asn	Thr	Trp	Asn	Thr	Pro	Glu	Phe	Lys	Glu	Phe	Thr	Gly	Val	Lys	195	200		205
Leu	Pro	Glu	Glu	Leu	Arg	Asn	Gln	Ile	Leu	Glu	Glu	Phe	Glu	Lys	Phe	210	215		220
Lys	Glu	Lys	Leu	Asp	Arg	Ile	Arg	Lys	Asn	His	Pro	Gly	Phe	Gly	Thr	225	230		240
Ile	His	Leu	Val	Gly	His	Ala	His	Ile	Asp	Tyr	Ala	Trp	Leu	Trp	Pro	245	250		255
Val	Glu	Glu	Thr	Lys	Arg	Lys	Ile	Leu	Arg	Thr	Phe	Ala	Asn	Ser	Val	260	265		270
Leu	Leu	Ser	Lys	Leu	Tyr	Pro	Glu	Phe	Val	Tyr	Thr	Gln	Ser	Ser	Ala	275	280		285
Gln	Met	Tyr	Glu	Asp	Leu	Lys	Gln	Asn	Ser	Pro	Glu	Leu	Phe	Glu	Glu	290	295		300
Val	Arg	Lys	Leu	Val	Glu	Glu	Gly	Arg	Trp	Glu	Pro	Val	Gly	Gly	Met	305	310		320
Trp	Val	Glu	Ser	Asp	Cys	Asn	Val	Pro	Ser	Ile	Glu	Ser	Leu	Val	Arg	325	330		335
Gln	Phe	Tyr	Tyr	Gly	Gln	Lys	Phe	Phe	Glu	Arg	Glu	Phe	Gly	Lys	Lys	340	345		350
Ser	Lys	Val	Cys	Trp	Leu	Pro	Asp	Val	Phe	Gly	Phe	Ser	Trp	Val	Leu	355	360		365
Pro	Gln	Ile	Leu	Lys	Glu	Ala	Gly	Ile	Lys	Tyr	Phe	Val	Thr	Thr	Lys	370	375		380
Leu	Asn	Trp	Asn	Asp	Thr	Asn	Glu	Phe	Pro	Tyr	Asp	Leu	Cys	Arg	Trp	385	390		400
Arg	Gly	Ile	Asp	Gly	Ser	Glu	Val	Ile	Tyr	Phe	Ser	Phe	Lys	Asn	Pro	405	410		415
Asn	Glu	Gly	Tyr	Asn	Gly	Lys	Ile	Asp	Pro	Asp	Thr	Val	Tyr	Lys	Thr	420	425		430
Trp	Lys	Asn	Phe	Arg	Gln	Lys	Asp	Leu	Thr	Asn	Arg	Val	Leu	Leu	Ser	435	440		445
Phe	Gly	His	Gly	Asp	Gly	Gly	Gly	Gly	Pro	Thr	Glu	Glu	Met	Leu	Glu	450	455		460
Asn	Tyr	Glu	Val	Leu	Lys	Asp	Phe	Pro	Gly	Leu	Pro	His	Leu	Glu	Met	465	470		480
Gly	Thr	Val	Glu	Glu	Phe	Phe	Lys	Lys	Val	Glu	Ile	Asp	Glu	Glu	Leu	485	490		495
Pro	Val	Trp	Asp	Gly	Glu	Leu	Tyr	Leu	Glu	Leu	His	Arg	Gly	Thr	Tyr	500	505		510
Thr	Ser	Gln	Phe	Arg	Thr	Lys	Lys	Leu	His	Lys	Glu	Ala	Glu	Asp	Ser	515	520		525
Leu	Tyr	Leu	Ala	Glu	Leu	Ile	Ser	Ala	Phe	Thr	Asp	Lys	Asp	Phe	Ser	530	535		540
Asp	Glu	Ile	Asp	Glu	Leu	Trp	Lys	Ile	Leu	Leu	Arg	Asn	Glu	Phe	His	545	550		560
Asp	Ile	Leu	Pro	Gly	Ser	Ser	Ile	Lys	Glu	Val	Tyr	Glu	Asp	Thr	Glu	565	570		575
Lys	Glu	Leu	Arg	His	Val	Ile	Glu	Lys	Ser	Lys	Asp	Ile	Val	Ile	Glu	580	585		590
Ser	Leu	Lys	Val	Leu	Ser	Ser	Glu	Asn	Lys	Asp	Val	Leu	Thr	Ile	Leu	595	600		605
Asn	Ala	Ser	Ser	Phe	Pro	Lys	Lys	Cys	Leu	Phe	Phe	Leu	Asn	Glu	Asp	610	615		620
Leu	Ala	Ile	Ser	Phe	Glu	Gly	Glu	Ala	Leu	Leu	Lys	Gln	Lys	Thr	His				

625					630					635					640
Asp	Gly	Arg	Tyr	Val	Tyr	Phe	Ile	Asp	Arg	Glu	Ile	Pro	Pro	Phe	Thr
				645					650					655	
Lys	Val	Glu	Leu	Lys	Val	Arg	Lys	Ala	Thr	Ser	Glu	Glu	Thr	Pro	Ser
			660					665					670		
Glu	Leu	Arg	Glu	Thr	Asn	Ile	Met	Glu	Asn	Glu	Phe	Leu	Arg	Val	His
		675				680				685					
Val	Asn	Asp	Asp	Gly	Thr	Ile	Gln	Ile	Tyr	Asp	Lys	Glu	Leu	Asp	Arg
	690				695					700					
Tyr	Val	Phe	Glu	Glu	Lys	Gly	Asn	Ile	Leu	Lys	Leu	His	Lys	Asn	Ile
705					710					715					720
Pro	Ala	Tyr	Trp	Asp	Asn	Trp	Asp	Ile	Ala	Glu	Asn	Val	Glu	Lys	Thr
			725						730					735	
Gly	Tyr	Thr	Leu	Arg	Ala	Lys	Asn	Ile	Glu	Lys	Ile	Glu	Ser	Gly	Pro
		740						745					750		
Val	Arg	Glu	Val	Ile	Arg	Val	Glu	His	Glu	Ser	Glu	Gly	Ser	Arg	Ile
	755					760					765				
Thr	Gln	His	Tyr	Ile	Leu	Tyr	Arg	Lys	Ser	Arg	Arg	Leu	Asp	Ile	Glu
	770				775					780					
Thr	Lys	Val	Asp	Trp	His	Thr	Arg	Arg	Ala	Leu	Leu	Arg	Ala	Tyr	Phe
785				790					795						800
Pro	Thr	Thr	Val	Leu	Ser	Arg	Lys	Ala	Arg	Phe	Asp	Ile	Ser	Gly	Gly
			805					810						815	
Phe	Ile	Glu	Arg	Pro	Thr	His	Arg	Asn	Thr	Ser	Phe	Glu	Gln	Ala	Arg
		820					825						830		
Phe	Glu	Val	Pro	Phe	His	Arg	Trp	Met	Asp	Leu	Ser	Gln	Thr	Asp	Phe
	835					840					845				
Gly	Val	Ser	Ile	Leu	Asn	Asp	Gly	Lys	Tyr	Gly	Gly	Ser	Val	His	Gln
	850				855					860					
Gly	Ile	Met	Ala	Leu	Ser	Leu	Ile	Lys	Ala	Gly	Ile	Phe	Pro	Asp	Phe
865				870					875						880
Leu	Cys	Asp	Glu	Gly	Glu	His	Thr	Phe	Thr	Tyr	Ser	Val	Tyr	Val	His
			885				890						895		
Pro	Gly	Asp	Ser	Leu	Arg	Asp	Val	Val	Lys	Gly	Ser	Glu	Asp	Leu	Asn
		900					905						910		
Arg	Ser	Phe	Ile	Val	His	Arg	Gly	Val	Leu	Asn	Leu	Pro	Ser	Pro	Leu
	915						920						925		
Leu	Glu	Ile	Ser	Pro	Gln	Asn	Phe	Arg	Leu	Thr	Ser	Leu	Arg	Arg	Val
	930				935						940				
Lys	Asp	Lys	Ile	Val	Leu	Arg	Leu	Val	Glu	Ile	Phe	Gly	Thr	Ser	Gly
945				950					955						960
Lys	Leu	Ser	Ile	Lys	Leu	Pro	Trp	His	Gly	Glu	Ile	Tyr	Gln	Thr	Asn
		965						970						975	
Val	Leu	Glu	Glu	Lys	Lys	Gln	Lys	Val	Thr	Phe	Pro	Val	Val	Tyr	His
		980					985						990		
Pro	Phe	Lys	Ile	Tyr	Thr	Phe	Val	Val	Glu	Gly					
	995						1000								

<210> 39

<211> 2337

<212> DNA

<213> Thermotoga maritima

<220>

<221> CDS

<222> (1)...(2337)

<223> clone # 6GC18

<400> 39

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 Met Glu Leu Tyr Arg Asp Pro Ser Gln Pro Ile Glu Val Arg Val Arg

1	5	10	15	
gat ctt ctt tcc aga atg acg ctg gaa gag aaa gtg gcc cag ctt ggg Asp Leu Leu Ser Arg Met Thr Leu Glu Glu Lys Val Ala Gln Leu Gly	20	25	30	96
tct gtc tgg ggt tac gaa ctg ata gac gag agg gga aag ttc agt aga Ser Val Trp Gly Tyr Glu Leu Ile Asp Glu Arg Gly Lys Phe Ser Arg	35	40	45	144
gaa aaa gca aaa gaa ctc ctc aaa aat ggt ata ggc cag atc aca agg Glu Lys Ala Lys Glu Leu Leu Lys Asn Gly Ile Gly Gln Ile Thr Arg	50	55	60	192
cct ggt gga tca acg aac ctt gaa cct caa gaa gcc gcg gaa ctt gtg Pro Gly Gly Ser Thr Asn Leu Glu Pro Gln Glu Ala Ala Glu Leu Val	65	70	75	240
aac gaa ata cag aga ttt ctt gtg gaa gaa aca cgc ctt gga att cct Asn Glu Ile Gln Arg Phe Leu Val Glu Glu Thr Arg Leu Gly Ile Pro	85	90	95	288
gcg atg ata cac gaa gaa tgt ctc acc ggt tac atg gga ctt gga gga Ala Met Ile His Glu Glu Cys Leu Thr Gly Tyr Met Gly Leu Gly Gly	100	105	110	336
acc aac ttc cct cag gcg ata gca atg gcg agt aca tgg gat cca gat Thr Asn Phe Pro Gln Ala Ile Ala Met Ala Ser Thr Trp Asp Pro Asp	115	120	125	384
ctc ata gaa aaa atg acc acc gcc gtc aga gag gat atg aga aag ata Leu Ile Glu Lys Met Thr Thr Ala Val Arg Glu Asp Met Arg Lys Ile	130	135	140	432
ggg gca cat cag ggt ctc gca cct gtt ctg gat gtc gca aga gat cca Gly Ala His Gln Gly Leu Ala Pro Val Leu Asp Val Ala Arg Asp Pro	145	150	155	480
agg tgg ggg aga aca gaa gag acg ttc gga gaa tct ccc tat ctg gtg Arg Trp Gly Arg Thr Glu Glu Thr Phe Gly Glu Ser Pro Tyr Leu Val	165	170	175	528
gcg agg atg gga gtc tct tac gtg aaa ggc ctc cag ggg gaa gat atc Ala Arg Met Gly Val Ser Tyr Val Lys Gly Leu Gln Gly Glu Asp Ile	180	185	190	576
aaa aaa ggt gtc gtt gcc aca gtg aaa cac ttc gcc gga tac agc gct Lys Lys Gly Val Val Ala Thr Val Lys His Phe Ala Gly Tyr Ser Ala	195	200	205	624
tct gaa ggt gga aag aac tgg gca cca acg aac att ccg gag agg gaa Ser Glu Gly Gly Lys Asn Trp Ala Pro Thr Asn Ile Pro Glu Arg Glu	210	215	220	672
ttc aaa gag gtc ttt ctc ttt ccg ttc gaa gcg gcc gtt aaa gaa gcg Phe Lys Glu Val Phe Leu Phe Pro Phe Glu Ala Ala Val Lys Glu Ala	225	230	235	720
aat gtg ctt tct gtg atg aac tcc tac agc gaa ata gac ggt gtc cca Asn Val Leu Ser Val Met Asn Ser Tyr Ser Glu Ile Asp Gly Val Pro	245	250	255	768

tgt gca gcg aac agg aaa ctc ctc aca gac att ctc aga aaa gac tgg Cys Ala Ala Asn Arg Lys Leu Leu Thr Asp Ile Leu Arg Lys Asp Trp 260 265 270	816
gga ttc gaa gga atc gtc gtt tct gac tat ttt gct gtg aaa gtt ctg Gly Phe Glu Gly Ile Val Val Ser Asp Tyr Phe Ala Val Lys Val Leu 275 280 285	864
gaa gat tat cac aga ata gca agg gat aag tca gaa gcc gca aga ctc Glu Asp Tyr His Arg Ile Ala Arg Asp Lys Ser Glu Ala Ala Arg Leu 290 295 300	912
gca ctt gaa gcg ggg ata gat gtt gaa ctt ccg aag aca gaa tgt tat Ala Leu Glu Ala Gly Ile Asp Val Glu Leu Pro Lys Thr Glu Cys Tyr 305 310 315 320	960
caa tat ttg aaa gac ctt gtt gaa aaa ggc atc atc tcc gaa gct ttg Gln Tyr Leu Lys Asp Leu Val Glu Lys Gly Ile Ile Ser Glu Ala Leu 325 330 335	1008
atc gac gag gca gtc acc agg gtg ctg agg ctg aag ttc atg ctc ggg Ile Asp Glu Ala Val Thr Arg Val Leu Arg Leu Lys Phe Met Leu Gly 340 345 350	1056
ctc ttc gaa aat ccc tac gtt gag gtg gaa aaa gca aag ata gaa agt Leu Phe Glu Asn Pro Tyr Val Glu Val Glu Lys Ala Lys Ile Glu Ser 355 360 365	1104
cac aga gac atc gca ctc gag ata gca agg aaa tcc att atc ctt ctc His Arg Asp Ile Ala Leu Glu Ile Ala Arg Lys Ser Ile Ile Leu Leu 370 375 380	1152
aag aat gat gga att ctg cct ctt cag aaa aac aaa aaa gtt gcc ctg Lys Asn Asp Gly Ile Leu Pro Leu Gln Lys Asn Lys Lys Val Ala Leu 385 390 395 400	1200
atc gga ccg aac gcg ggt gag gtg aga aat ctc ctc gga gat tac atg Ile Gly Pro Asn Ala Gly Glu Val Arg Asn Leu Leu Gly Asp Tyr Met 405 410 415	1248
tac ctt gca cac ata agg gct ctc ctc gac aac ata gac gac gtc ttt Tyr Leu Ala His Ile Arg Ala Leu Leu Asp Asn Ile Asp Asp Val Phe 420 425 430	1296
gga aat cct cag atc ccg aga gaa aac tac gaa aga ctg aag aag agc Gly Asn Pro Gln Ile Pro Arg Glu Asn Tyr Glu Arg Leu Lys Lys Ser 435 440 445	1344
ata gaa gaa cat atg aag agc att ccg agt gtt ctc gat gcc ttc aaa Ile Glu Glu His Met Lys Ser Ile Pro Ser Val Leu Asp Ala Phe Lys 450 455 460	1392
gaa gaa ggg atc gaa ttc gaa tat gca aaa ggc tgt gaa gtg aca ggg Glu Glu Gly Ile Glu Phe Glu Tyr Ala Lys Gly Cys Glu Val Thr Gly 465 470 475 480	1440
gaa gac aga agc ggt ttc gaa gag gcg ata gaa att gca aag aaa tcc Glu Asp Arg Ser Gly Phe Glu Glu Ala Ile Glu Ile Ala Lys Lys Ser 485 490 495	1488

gac gtt gcc atc gtt gtc gta ggg gac aaa tct gga ctc acc ctt gac Asp Val Ala Ile Val Val Val Gly Asp Lys Ser Gly Leu Thr Leu Asp 500 505 510	1536
tgc aca acc ggt gag tcc aga gac atg gca aac ctc aag ctt cca gga Cys Thr Thr Gly Glu Ser Arg Asp Met Ala Asn Leu Lys Leu Pro Gly 515 520 525	1584
gtc cag gaa gaa ctc gtc ctc gaa gtt gca aag aca gga aaa ccc gtc Val Gln Glu Glu Leu Val Leu Glu Val Ala Lys Thr Gly Lys Pro Val 530 535 540	1632
gtt ctt gtc ctc atc acg gga aga ccc tat tca ctc aaa aac gtc gtc Val Leu Val Leu Ile Thr Gly Arg Pro Tyr Ser Leu Lys Asn Val Val 545 550 555 560	1680
gac aag gtg aac gcg atc ctt cag gtg tgg ctt cct gga gaa gcg gga Asp Lys Val Asn Ala Ile Leu Gln Val Trp Leu Pro Gly Glu Ala Gly 565 570 575	1728
gga aga gcg atc gtt gac atc atc tat gga aag gtg aat ccc tct gga Gly Arg Ala Ile Val Asp Ile Ile Tyr Gly Lys Val Asn Pro Ser Gly 580 585 590	1776
aaa ctc ccg atc agc ttt cca aga agc gct ggt cag att cct gtc ttc Lys Leu Pro Ile Ser Phe Pro Arg Ser Ala Gly Gln Ile Pro Val Phe 595 600 605	1824
cac tac gtc aaa cca tcc ggg gga agg tct cac tgg cac gga gac tac His Tyr Val Lys Pro Ser Gly Gly Arg Ser His Trp His Gly Asp Tyr 610 615 620	1872
gtg gat gag agc aca aag cct ctc ttc ccg ttt ggg cac ggt ttg tct Val Asp Glu Ser Thr Lys Pro Leu Phe Pro Phe Gly His Gly Leu Ser 625 630 635 640	1920
tac acg aag ttc gag tac agc aac ctc aga atc gag ccg aag gaa gtg Tyr Thr Lys Phe Glu Tyr Ser Asn Leu Arg Ile Glu Pro Lys Glu Val 645 650 655	1968
cca ccg gcc ggc gaa gtg gtg ata aag gtg gac gtg gaa aac atc gga Pro Pro Ala Gly Glu Val Val Ile Lys Val Asp Val Glu Asn Ile Gly 660 665 670	2016
gac aga gac gga gac gag gtg gtt caa ctt tac atc ggt cgt gag ttt Asp Arg Asp Gly Asp Glu Val Val Gln Leu Tyr Ile Gly Arg Glu Phe 675 680 685	2064
gca agc gtc aca agg cct gtg aaa gag ctg aag ggc ttc aag agg gtt Ala Ser Val Thr Arg Pro Val Lys Glu Leu Lys Gly Phe Lys Arg Val 690 695 700	2112
tct ttg aag gcg aaa gag aag aag act gtt gtg ttc agg ctt cac atg Ser Leu Lys Ala Lys Glu Lys Lys Thr Val Val Phe Arg Leu His Met 705 710 715 720	2160
gac gtg ctc gcc tac tac aac aga gac atg aaa ctc gtg gtt gaa ccc Asp Val Leu Ala Tyr Tyr Asn Arg Asp Met Lys Leu Val Val Glu Pro 725 730 735	2208
ggg gag ttc aaa gtg atg gtg gga agc tct tct gaa gac atc aga ctc	2256

Gly Glu Phe Lys Val Met Val Gly Ser Ser Ser Glu Asp Ile Arg Leu
740 745 750

aca ggt tct ttc tcc gtc gtc ggt gaa aaa aga gaa gtg gtg gga atg 2304
Thr Gly Ser Phe Ser Val Val Gly Glu Lys Arg Glu Val Val Gly Met
755 760 765

agg aaa ttc ttc acg gaa gcc tgc gag gag tga 2337
Arg Lys Phe Phe Thr Glu Ala Cys Glu Glu *
770 775

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20 25 30
Ser Val Trp Gly Tyr Glu Leu Ile Asp Glu Arg Gly Lys Phe Ser Arg
35 40 45
Glu Lys Ala Lys Glu Leu Leu Lys Asn Gly Ile Gly Gln Ile Thr Arg
50 55 60
Pro Gly Gly Ser Thr Asn Leu Glu Pro Gln Glu Ala Ala Glu Leu Val
65 70 75 80
Asn Glu Ile Gln Arg Phe Leu Val Glu Glu Thr Arg Leu Gly Ile Pro
85 90 95
Ala Met Ile His Glu Glu Cys Leu Thr Gly Tyr Met Gly Leu Gly Gly
100 105 110

Thr Asn Phe Pro Gln Ala Ile Ala Met Ala Ser Thr Trp Asp Pro Asp
115 120 125
Leu Ile Glu Lys Met Thr Thr Ala Val Arg Glu Asp Met Arg Lys Ile
130 135 140
Gly Ala His Gln Gly Leu Ala Pro Val Leu Asp Val Ala Arg Asp Pro
145 150 155 160
Arg Trp Gly Arg Thr Glu Glu Thr Phe Gly Glu Ser Pro Tyr Leu Val
165 170 175
Ala Arg Met Gly Val Ser Tyr Val Lys Gly Leu Gln Gly Glu Asp Ile
180 185 190
Lys Lys Gly Val Val Ala Thr Val Lys His Phe Ala Gly Tyr Ser Ala
195 200 205
Ser Glu Gly Gly Lys Asn Trp Ala Pro Thr Asn Ile Pro Glu Arg Glu
210 215 220
Phe Lys Glu Val Phe Leu Phe Pro Phe Glu Ala Ala Val Lys Glu Ala
225 230 235 240
Asn Val Leu Ser Val Met Asn Ser Tyr Ser Glu Ile Asp Gly Val Pro
245 250 255
Cys Ala Ala Asn Arg Lys Leu Leu Thr Asp Ile Leu Arg Lys Asp Trp
260 265 270
Gly Phe Glu Gly Ile Val Val Ser Asp Tyr Phe Ala Val Lys Val Leu
275 280 285
Glu Asp Tyr His Arg Ile Ala Arg Asp Lys Ser Glu Ala Ala Arg Leu
290 295 300
Ala Leu Glu Ala Gly Ile Asp Val Glu Leu Pro Lys Thr Glu Cys Tyr
305 310 315 320
Gln Tyr Leu Lys Asp Leu Val Glu Lys Gly Ile Ile Ser Glu Ala Leu
325 330 335
Ile Asp Glu Ala Val Thr Arg Val Leu Arg Leu Lys Phe Met Leu Gly

			340					345					350		
Leu	Phe	Glu	Asn	Pro	Tyr	Val	Glu	Val	Glu	Lys	Ala	Lys	Ile	Glu	Ser
		355					360					365			
His	Arg	Asp	Ile	Ala	Leu	Glu	Ile	Ala	Arg	Lys	Ser	Ile	Ile	Leu	Leu
	370					375					380				
Lys	Asn	Asp	Gly	Ile	Leu	Pro	Leu	Gln	Lys	Asn	Lys	Lys	Val	Ala	Leu
385					390					395					400
Ile	Gly	Pro	Asn	Ala	Gly	Glu	Val	Arg	Asn	Leu	Leu	Gly	Asp	Tyr	Met
			405						410					415	
Tyr	Leu	Ala	His	Ile	Arg	Ala	Leu	Leu	Asp	Asn	Ile	Asp	Asp	Val	Phe
			420					425					430		
Gly	Asn	Pro	Gln	Ile	Pro	Arg	Glu	Asn	Tyr	Glu	Arg	Leu	Lys	Lys	Ser
		435					440					445			
Ile	Glu	Glu	His	Met	Lys	Ser	Ile	Pro	Ser	Val	Leu	Asp	Ala	Phe	Lys
	450					455					460				
Glu	Glu	Gly	Ile	Glu	Phe	Glu	Tyr	Ala	Lys	Gly	Cys	Glu	Val	Thr	Gly
465					470					475					480
Glu	Asp	Arg	Ser	Gly	Phe	Glu	Glu	Ala	Ile	Glu	Ile	Ala	Lys	Lys	Ser
				485					490					495	
Asp	Val	Ala	Ile	Val	Val	Val	Gly	Asp	Lys	Ser	Gly	Leu	Thr	Leu	Asp
			500					505					510		
Cys	Thr	Thr	Gly	Glu	Ser	Arg	Asp	Met	Ala	Asn	Leu	Lys	Leu	Pro	Gly
		515					520					525			
Val	Gln	Glu	Glu	Leu	Val	Leu	Glu	Val	Ala	Lys	Thr	Gly	Lys	Pro	Val
	530					535					540				
Val	Leu	Val	Leu	Ile	Thr	Gly	Arg	Pro	Tyr	Ser	Leu	Lys	Asn	Val	Val
545					550					555					560
Asp	Lys	Val	Asn	Ala	Ile	Leu	Gln	Val	Trp	Leu	Pro	Gly	Glu	Ala	Gly
			565						570					575	
Gly	Arg	Ala	Ile	Val	Asp	Ile	Ile	Tyr	Gly	Lys	Val	Asn	Pro	Ser	Gly
			580					585					590		
Lys	Leu	Pro	Ile	Ser	Phe	Pro	Arg	Ser	Ala	Gly	Gln	Ile	Pro	Val	Phe
		595					600					605			
His	Tyr	Val	Lys	Pro	Ser	Gly	Gly	Arg	Ser	His	Trp	His	Gly	Asp	Tyr
	610					615					620				
Val	Asp	Glu	Ser	Thr	Lys	Pro	Leu	Phe	Pro	Phe	Gly	His	Gly	Leu	Ser
625					630					635					640
Tyr	Thr	Lys	Phe	Glu	Tyr	Ser	Asn	Leu	Arg	Ile	Glu	Pro	Lys	Glu	Val
			645						650					655	
Pro	Pro	Ala	Gly	Glu	Val	Val	Ile	Lys	Val	Asp	Val	Glu	Asn	Ile	Gly
			660					665					670		
Asp	Arg	Asp	Gly	Asp	Glu	Val	Val	Gln	Leu	Tyr	Ile	Gly	Arg	Glu	Phe
		675					680					685			
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<210> 41
<211> 2043
<212> DNA
<213> Thermotoga maritima
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<220>
 <221> CDS
 <222> (1)...(2043)
 <223> clone # 6GP2

<400> 41

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ttc ctt tta ttg atc gtt gag ctc tct ttc gtt ctc ttt gca agt gac	96
Phe Leu Leu Leu Ile Val Glu Leu Ser Phe Val Leu Phe Ala Ser Asp	
20 25 30	
gag ttc gtg aaa gtg gaa aac gga aaa ttc gct ctg aac gga aaa gaa	144
Glu Phe Val Lys Val Glu Asn Gly Lys Phe Ala Leu Asn Gly Lys Glu	
35 40 45	
ttc aga ttc att gga agc aac aac tac tac atg cac tac aag agc aac	192
Phe Arg Phe Ile Gly Ser Asn Asn Tyr Tyr Met His Tyr Lys Ser Asn	
50 55 60	
gga atg ata gac agt gtt ctg gag agt gcc aga gac atg ggt ata aag	240
Gly Met Ile Asp Ser Val Leu Glu Ser Ala Arg Asp Met Gly Ile Lys	
65 70 75 80	
gtc ctc aga atc tgg ggt ttc ctc gac ggg gag agt tac tgc aga gac	288
Val Leu Arg Ile Trp Gly Phe Leu Asp Gly Glu Ser Tyr Cys Arg Asp	
85 90 95	
aag aac acc tac atg cat cct gag ccc ggt gtt ttc ggg gtg cca gaa	336
Lys Asn Thr Tyr Met His Pro Glu Pro Gly Val Phe Gly Val Pro Glu	
100 105 110	
gga ata tcg aac gcc cag agc ggt ttc gaa aga ctc gac tac aca gtt	384
Gly Ile Ser Asn Ala Gln Ser Gly Phe Glu Arg Leu Asp Tyr Thr Val	
115 120 125	
gcg aaa gcg aaa gaa ctc ggt ata aaa ctt gtc att gtt ctt gtg aac	432
Ala Lys Ala Lys Glu Leu Gly Ile Lys Leu Val Ile Val Leu Val Asn	
130 135 140	
aac tgg gac gac ttc ggt gga atg aac cag tac gtg agg tgg ttt gga	480
Asn Trp Asp Asp Phe Gly Gly Met Asn Gln Tyr Val Arg Trp Phe Gly	
145 150 155 160	
gga acc cat cac gac gat ttc tac aga gat gag aag atc aaa gaa gag	528
Gly Thr His His Asp Asp Phe Tyr Arg Asp Glu Lys Ile Lys Glu Glu	
165 170 175	
tac aaa aag tac gtc tcc ttt ctc gta aac cat gtc aat acc tac acg	576
Tyr Lys Lys Tyr Val Ser Phe Leu Val Asn His Val Asn Thr Tyr Thr	
180 185 190	
gga gtt cct tac agg gaa gag ccc acc atc atg gcc tgg gag ctt gca	624
Gly Val Pro Tyr Arg Glu Glu Pro Thr Ile Met Ala Trp Glu Leu Ala	
195 200 205	
aac gaa ccg cgc tgt gag acg gac aaa tcg ggg aac acg ctc gtt gag	672
Asn Glu Pro Arg Cys Glu Thr Asp Lys Ser Gly Asn Thr Leu Val Glu	
210 215 220	

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Trp Val Lys Glu Met Ser Ser Tyr Ile Lys Ser Leu Asp Pro Asn His	
225 230 235 240	
ctc gtg gct gtg ggg gac gaa gga ttc ttc agc aac tac gaa gga ttc	768
Leu Val Ala Val Gly Asp Glu Gly Phe Phe Ser Asn Tyr Glu Gly Phe	
245 250 255	
aaa cct tac ggt gga gaa gcc gag tgg gcc tac aac ggc tgg tcc ggt	816
Lys Pro Tyr Gly Gly Glu Ala Glu Trp Ala Tyr Asn Gly Trp Ser Gly	
260 265 270	
gtt gac tgg aag aag ctc ctt tcg ata gag acg gtg gac ttc ggc acg	864
Val Asp Trp Lys Lys Leu Leu Ser Ile Glu Thr Val Asp Phe Gly Thr	
275 280 285	
ttc cac ctc tat ccg tcc cac tgg ggt gtc agt cca gag aac tat gcc	912
Phe His Leu Tyr Pro Ser His Trp Gly Val Ser Pro Glu Asn Tyr Ala	
290 295 300	
cag tgg gga gcg aag tgg ata gaa gac cac ata aag atc gca aaa gag	960
Gln Trp Gly Ala Lys Trp Ile Glu Asp His Ile Lys Ile Ala Lys Glu	
305 310 315 320	
atc gga aaa ccc gtt gtt ctg gaa gaa tat gga att cca aag agt gcg	1008
Ile Gly Lys Pro Val Val Leu Glu Glu Tyr Gly Ile Pro Lys Ser Ala	
325 330 335	
cca gtt aac aga acg gcc atc tac aga ctc tgg aac gat ctg gtc tac	1056
Pro Val Asn Arg Thr Ala Ile Tyr Arg Leu Trp Asn Asp Leu Val Tyr	
340 345 350	
gat ctc ggt gga gat gga gcg atg ttc tgg atg ctc gcg gga atc ggg	1104
Asp Leu Gly Gly Asp Gly Ala Met Phe Trp Met Leu Ala Gly Ile Gly	
355 360 365	
gaa ggt tcg gac aga gac gag aga ggg tac tat ccg gac tac gac ggt	1152
Glu Gly Ser Asp Arg Asp Glu Arg Gly Tyr Tyr Pro Asp Tyr Asp Gly	
370 375 380	
ttc aga ata gtg aac gac gac agt cca gaa gcg gaa ctg ata aga gaa	1200
Phe Arg Ile Val Asn Asp Asp Ser Pro Glu Ala Glu Leu Ile Arg Glu	
385 390 395 400	
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Tyr Ala Lys Leu Phe Asn Thr Gly Glu Asp Ile Arg Glu Asp Thr Cys	
405 410 415	
tct ttc atc ctt cca aaa gac ggc atg gag atc aaa aag acc gtg gaa	1296
Ser Phe Ile Leu Pro Lys Asp Gly Met Glu Ile Lys Lys Thr Val Glu	
420 425 430	
gtg agg gct ggt gtt ttc gac tac agc aac acg ttt gaa aag ttg tct	1344
Val Arg Ala Gly Val Phe Asp Tyr Ser Asn Thr Phe Glu Lys Leu Ser	
435 440 445	
gtc aaa gtc gaa gat ctg gtt ttt gaa aat gag ata gag cat ctc gga	1392
Val Lys Val Glu Asp Leu Val Phe Glu Asn Glu Ile Glu His Leu Gly	
450 455 460	

tac gga att tac ggc ttt gat ctc gac aca acc cgg atc ccg gat gga Tyr Gly Ile Tyr Gly Phe Asp Leu Asp Thr Thr Arg Ile Pro Asp Gly 465 470 475 480	1440
gaa cat gaa atg ttc ctt gaa ggc cac ttt cag gga aaa acg gtg aaa Glu His Glu Met Phe Leu Glu Gly His Phe Gln Gly Lys Thr Val Lys 485 490 495	1488
gac tct atc aaa gcg aaa gtg gtg aac gaa gca cgg tac gtg ctc gca Asp Ser Ile Lys Ala Lys Val Val Asn Glu Ala Arg Tyr Val Leu Ala 500 505 510	1536
gag gaa gtt gat ttt tcc tct cca gaa gag gtg aaa aac tgg tgg aac Glu Glu Val Asp Phe Ser Ser Pro Glu Glu Val Lys Asn Trp Trp Asn 515 520 525	1584
agc gga acc tgg cag gca gag ttc ggg tca cct gac att gaa tgg aac Ser Gly Thr Trp Gln Ala Glu Phe Gly Ser Pro Asp Ile Glu Trp Asn 530 535 540	1632
ggg gag gtg gga aat gga gca ctg cag ctg aac gtg aaa ctg ccc gga Gly Glu Val Gly Asn Gly Ala Leu Gln Leu Asn Val Lys Leu Pro Gly 545 550 555 560	1680
aag agc gac tgg gaa gaa gtg aga gta gca agg aag ttc gaa aga ctc Lys Ser Asp Trp Glu Glu Val Arg Val Ala Arg Lys Phe Glu Arg Leu 565 570 575	1728
tca gaa tgt gag atc ctc gag tac gac atc tac att cca aac gtc gag Ser Glu Cys Glu Ile Leu Glu Tyr Asp Ile Tyr Ile Pro Asn Val Glu 580 585 590	1776
gga ctc aag gga agg ttg agg ccg tac gcg gtt ctg aac ccc ggc tgg Gly Leu Lys Gly Arg Leu Arg Pro Tyr Ala Val Leu Asn Pro Gly Trp 595 600 605	1824
gtg aag ata ggc ctc gac atg aac aac gcg aac gtg gaa agt gcg gag Val Lys Ile Gly Leu Asp Met Asn Asn Ala Asn Val Glu Ser Ala Glu 610 615 620	1872
atc atc act ttc ggc gga aaa gag tac aga aga ttc cat gta aga att Ile Ile Thr Phe Gly Gly Lys Glu Tyr Arg Arg Phe His Val Arg Ile 625 630 635 640	1920
gag ttc gac aga aca gcg ggc gtg aaa gaa ctt cac ata gga gtt gtc Glu Phe Asp Arg Thr Ala Gly Val Lys Glu Leu His Ile Gly Val Val 645 650 655	1968
ggg gat cat ctg agg tac gat gga ccg att ttc atc gat aat gtg aga Gly Asp His Leu Arg Tyr Asp Gly Pro Ile Phe Ile Asp Asn Val Arg 660 665 670	2016
ctt tat aaa aga aca gga ggt atg tga Leu Tyr Lys Arg Thr Gly Gly Met * 675 680	2043

<210> 42

<211> 680

<212> PRT

<213> Thermotoga maritima

<400> 42

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		20						25					30		
Glu	Phe	Val	Lys	Val	Glu	Asn	Gly	Lys	Phe	Ala	Leu	Asn	Gly	Lys	Glu
		35					40					45			
Phe	Arg	Phe	Ile	Gly	Ser	Asn	Asn	Tyr	Tyr	Met	His	Tyr	Lys	Ser	Asn
	50					55					60				
Gly	Met	Ile	Asp	Ser	Val	Leu	Glu	Ser	Ala	Arg	Asp	Met	Gly	Ile	Lys
65					70				75						80
Val	Leu	Arg	Ile	Trp	Gly	Phe	Leu	Asp	Gly	Glu	Ser	Tyr	Cys	Arg	Asp
			85						90				95		
Lys	Asn	Thr	Tyr	Met	His	Pro	Glu	Pro	Gly	Val	Phe	Gly	Val	Pro	Glu
		100						105					110		
Gly	Ile	Ser	Asn	Ala	Gln	Ser	Gly	Phe	Glu	Arg	Leu	Asp	Tyr	Thr	Val
	115						120					125			
Ala	Lys	Ala	Lys	Glu	Leu	Gly	Ile	Lys	Leu	Val	Ile	Val	Leu	Val	Asn
	130					135					140				
Asn	Trp	Asp	Asp	Phe	Gly	Gly	Met	Asn	Gln	Tyr	Val	Arg	Trp	Phe	Gly
145					150				155						160
Gly	Thr	His	His	Asp	Asp	Phe	Tyr	Arg	Asp	Glu	Lys	Ile	Lys	Glu	Glu
			165					170					175		
Tyr	Lys	Lys	Tyr	Val	Ser	Phe	Leu	Val	Asn	His	Val	Asn	Thr	Tyr	Thr
		180					185						190		
Gly	Val	Pro	Tyr	Arg	Glu	Glu	Pro	Thr	Ile	Met	Ala	Trp	Glu	Leu	Ala
	195						200					205			
Asn	Glu	Pro	Arg	Cys	Glu	Thr	Asp	Lys	Ser	Gly	Asn	Thr	Leu	Val	Glu
	210					215					220				
Trp	Val	Lys	Glu	Met	Ser	Ser	Tyr	Ile	Lys	Ser	Leu	Asp	Pro	Asn	His
225				230					235						240
Leu	Val	Ala	Val	Gly	Asp	Glu	Gly	Phe	Phe	Ser	Asn	Tyr	Glu	Gly	Phe
				245				250					255		
Lys	Pro	Tyr	Gly	Gly	Glu	Ala	Glu	Trp	Ala	Tyr	Asn	Gly	Trp	Ser	Gly
		260						265					270		
Val	Asp	Trp	Lys	Lys	Leu	Leu	Ser	Ile	Glu	Thr	Val	Asp	Phe	Gly	Thr
	275						280					285			
Phe	His	Leu	Tyr	Pro	Ser	His	Trp	Gly	Val	Ser	Pro	Glu	Asn	Tyr	Ala
	290					295					300				
Gln	Trp	Gly	Ala	Lys	Trp	Ile	Glu	Asp	His	Ile	Lys	Ile	Ala	Lys	Glu
305				310					315						320
Ile	Gly	Lys	Pro	Val	Val	Leu	Glu	Glu	Tyr	Gly	Ile	Pro	Lys	Ser	Ala
			325						330					335	
Pro	Val	Asn	Arg	Thr	Ala	Ile	Tyr	Arg	Leu	Trp	Asn	Asp	Leu	Val	Tyr
		340						345					350		
Asp	Leu	Gly	Gly	Asp	Gly	Ala	Met	Phe	Trp	Met	Leu	Ala	Gly	Ile	Gly
	355					360					365				
Glu	Gly	Ser	Asp	Arg	Asp	Glu	Arg	Gly	Tyr	Tyr	Pro	Asp	Tyr	Asp	Gly
	370					375					380				
Phe	Arg	Ile	Val	Asn	Asp	Asp	Ser	Pro	Glu	Ala	Glu	Leu	Ile	Arg	Glu
385				390					395						400
Tyr	Ala	Lys	Leu	Phe	Asn	Thr	Gly	Glu	Asp	Ile	Arg	Glu	Asp	Thr	Cys
			405					410					415		
Ser	Phe	Ile	Leu	Pro	Lys	Asp	Gly	Met	Glu	Ile	Lys	Lys	Thr	Val	Glu
		420					425						430		
Val	Arg	Ala	Gly	Val	Phe	Asp	Tyr	Ser	Asn	Thr	Phe	Glu	Lys	Leu	Ser
	435						440					445			
Val	Lys	Val	Glu	Asp	Leu	Val	Phe	Glu	Asn	Glu	Ile	Glu	His	Leu	Gly
	450					455					460				
Tyr	Gly	Ile	Tyr	Gly	Phe	Asp	Leu	Asp	Thr	Thr	Arg	Ile	Pro	Asp	Gly

465		470		475		480
Glu His Glu Met Phe Leu Glu Gly His Phe Gln Gly Lys Thr Val Lys						
	485		490			495
Asp Ser Ile Lys Ala Lys Val Val Asn Glu Ala Arg Tyr Val Leu Ala						
	500		505			510
Glu Glu Val Asp Phe Ser Ser Pro Glu Glu Val Lys Asn Trp Trp Asn						
	515		520			525
Ser Gly Thr Trp Gln Ala Glu Phe Gly Ser Pro Asp Ile Glu Trp Asn						
	530		535			540
Gly Glu Val Gly Asn Gly Ala Leu Gln Leu Asn Val Lys Leu Pro Gly						
545		550		555		560
Lys Ser Asp Trp Glu Glu Val Arg Val Ala Arg Lys Phe Glu Arg Leu						
	565		570			575
Ser Glu Cys Glu Ile Leu Glu Tyr Asp Ile Tyr Ile Pro Asn Val Glu						
	580		585			590
Gly Leu Lys Gly Arg Leu Arg Pro Tyr Ala Val Leu Asn Pro Gly Trp						
	595		600			605
Val Lys Ile Gly Leu Asp Met Asn Asn Ala Asn Val Glu Ser Ala Glu						
	610		615			620
Ile Ile Thr Phe Gly Gly Lys Glu Tyr Arg Arg Phe His Val Arg Ile						
625		630		635		640
Glu Phe Asp Arg Thr Ala Gly Val Lys Glu Leu His Ile Gly Val Val						
	645		650			655
Gly Asp His Leu Arg Tyr Asp Gly Pro Ile Phe Ile Asp Asn Val Arg						
	660		665			670
Leu Tyr Lys Arg Thr Gly Gly Met						
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<210> 43

<211> 2712

<212> DNA

<213> Polyangium brachysporum

<220>

<221> CDS

<222> (1)...(2712)

<223> clone # 78GA1

<400> 43

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gcc gtg ctg tgt ctg gcc gtc gca ggc tgc ggt ggt ggt gat gac gac	96
Ala Val Leu Cys Leu Ala Val Ala Gly Cys Gly Gly Gly Asp Asp Asp	
20 25 30	

ggc gac gac aac ggc acc gcc ccc cag ccc gca cct ggt caa ccc gag	144
Gly Asp Asp Asn Gly Thr Ala Pro Gln Pro Ala Pro Gly Gln Pro Glu	
35 40 45	

ccc ccg act gac acc gtg ctg aaa gac tgg cct cgc atc aac agc agc	192
Pro Pro Thr Asp Thr Val Leu Lys Asp Trp Pro Arg Ile Asn Ser Ser	
50 55 60	

atc acc gcc gac gca gcg atc gaa agc cgc gtc aac tca ctc gtc gcg	240
Ile Thr Ala Asp Ala Ala Ile Glu Ser Arg Val Asn Ser Leu Val Ala	
65 70 75 80	

gcg atg acg ctg gaa gaa aaa gtc ggc cag atg acg cag gtc gaa atc	288
Ala Met Thr Leu Glu Glu Lys Val Gly Gln Met Thr Gln Val Glu Ile	

85								90					95					
cag	gag	gtg	acg	ccg	gag	gag	atc	cgg	cag	tac	cac	atc	ggc	tcc	gtg	336		
Gln	Glu	Val	Thr	Pro	Glu	Glu	Ile	Arg	Gln	Tyr	His	Ile	Gly	Ser	Val			
100								105				110						
ctc	aac	ggc	ggg	ggg	tcg	ttc	ccg	aag	cag	gac	aag	ggc	gcg	gcg	gtg	384		
Leu	Asn	Gly	Gly	Gly	Ser	Phe	Pro	Lys	Gln	Asp	Lys	Gly	Ala	Ala	Val			
115								120				125						
acc	gac	tgg	ctg	gcg	gtg	gcc	gac	gcc	ttg	tgg	gcc	gcg	tcg	atg	gat	432		
Thr	Asp	Trp	Leu	Ala	Val	Ala	Asp	Ala	Leu	Trp	Ala	Ala	Ser	Met	Asp			
130								135				140						
ccc	gcc	aag	ccg	cgg	cgc	atc	ccg	ctc	atc	tgg	ggc	acc	gac	gcc	gtc	480		
Pro	Ala	Lys	Pro	Arg	Arg	Ile	Pro	Leu	Ile	Trp	Gly	Thr	Asp	Ala	Val			
145				150				155				160						
cac	ggc	cac	aac	aac	gtc	aag	ggc	gcg	acc	atc	ttc	ccg	cac	aac	atc	528		
His	Gly	His	Asn	Asn	Val	Lys	Gly	Ala	Thr	Ile	Phe	Pro	His	Asn	Ile			
165								170				175						
ggc	ctg	ggc	gcc	gcg	cgc	gac	ccc	gac	ttg	gtc	gcc	cgc	atc	ggc	gcc	576		
Gly	Leu	Gly	Ala	Ala	Arg	Asp	Pro	Asp	Leu	Val	Ala	Arg	Ile	Gly	Ala			
180								185				190						
gcc	acg	gcg	ctg	gaa	gtg	gca	cgc	acc	ggc	atc	gac	tgg	gtg	ttc	gcg	624		
Ala	Thr	Ala	Leu	Glu	Val	Ala	Arg	Thr	Gly	Ile	Asp	Trp	Val	Phe	Ala			
195								200				205						
cca	acg	ctg	gcg	gtc	gtg	cgc	gac	gac	cgc	tgg	ggc	cgc	agc	tac	gaa	672		
Pro	Thr	Leu	Ala	Val	Val	Arg	Asp	Asp	Arg	Trp	Gly	Arg	Ser	Tyr	Glu			
210				215				220										
ggc	tat	tcg	gaa	gac	ccc	gaa	atc	gtc	gtc	tcc	tat	gcc	ggc	aag	atg	720		
Gly	Tyr	Ser	Glu	Asp	Pro	Glu	Ile	Val	Val	Ser	Tyr	Ala	Gly	Lys	Met			
225				230				235				240						
gtc	gaa	ggc	ctg	cag	ggc	cga	ttg	gcg	cag	gac	gcg	aag	gcc	aac	gag	768		
Val	Glu	Gly	Leu	Gln	Gly	Arg	Leu	Ala	Gln	Asp	Ala	Lys	Ala	Asn	Glu			
245								250				255						
aag	gtg	gtg	gcc	acc	gcc	aag	cat	ttc	gtc	ggc	gac	ggc	ggc	acc	gac	816		
Lys	Val	Val	Ala	Thr	Ala	Lys	His	Phe	Val	Gly	Asp	Gly	Gly	Thr	Asp			
260								265				270						
cag	ggc	aag	gac	cag	ggg	gtc	acc	cgg	gtc	acc	gag	cgc	gac	ctg	ttg	864		
Gln	Gly	Lys	Asp	Gln	Gly	Val	Thr	Arg	Val	Thr	Glu	Arg	Asp	Leu	Leu			
275								280				285						
aac	gtc	cat	gcg	cgc	ggc	tac	atc	ccc	gcg	ctc	gag	gcg	ggc	gcg	caa	912		
Asn	Val	His	Ala	Arg	Gly	Tyr	Ile	Pro	Ala	Leu	Glu	Ala	Gly	Ala	Gln			
290				295				300										
acc	gtg	atg	gcc	tcc	ttc	aac	agc	tgg	cag	gac	ccg	tcg	cag	ggc	gag	960		
Thr	Val	Met	Ala	Ser	Phe	Asn	Ser	Trp	Gln	Asp	Pro	Ser	Gln	Gly	Glu			
305				310				315				320						
ggc	gcc	aag	gcc	ttc	aag	atg	cat	ggc	agc	cgc	tac	ctg						

gcc ctc aag cag aag atg ggc ttc gac ggt ttc gtg gtg tcc gac tgg	1056
Ala Leu Lys Gln Lys Met Gly Phe Asp Gly Phe Val Val Ser Asp Trp	
340 345 350	
aac ggc atc ggc cag gtc acc acc gag aac agc aac gcg acg cgc aac	1104
Asn Gly Ile Gly Gln Val Thr Thr Glu Asn Ser Asn Ala Thr Arg Asn	
355 360 365	
tgc agc aac agc gac tgc ccc gag gcc atc aac gct ggc atc gac atg	1152
Cys Ser Asn Ser Asp Cys Pro Glu Ala Ile Asn Ala Gly Ile Asp Met	
370 375 380	
gtg atg gtg ccg tac cgg gcc gac tgg aag gcc ttc atc acc aac aca	1200
Val Met Val Pro Tyr Arg Ala Asp Trp Lys Ala Phe Ile Thr Asn Thr	
385 390 395 400	
att gca att gtc cgc aaa ggc gag atc gcg cag gag cgc atc gac aac	1248
Ile Ala Ile Val Arg Lys Gly Glu Ile Ala Gln Glu Arg Ile Asp Asn	
405 410 415	
gcg gtg cgg cgc atc ctg cgc gtc aag ttg cgc gcc ggt ctg ttc gac	1296
Ala Val Arg Arg Ile Leu Arg Val Lys Leu Arg Ala Gly Leu Phe Asp	
420 425 430	
aag ccc aca ccc tcc gcc cgt ctg gcc tcg cgc gag gtc ggc agc gcc	1344
Lys Pro Thr Pro Ser Ala Arg Leu Ala Ser Arg Glu Val Gly Ser Ala	
435 440 445	
gaa cac cgg gcg ctc gcg cgt gaa gcg gtg cgc aag tcg ttg gtg ctg	1392
Glu His Arg Ala Leu Ala Arg Glu Ala Val Arg Lys Ser Leu Val Leu	
450 455 460	
ttg aag aac aac ggc cgg gtg ctg ccg ctg gca cgc aat gcc aag gtc	1440
Leu Lys Asn Asn Gly Arg Val Leu Pro Leu Ala Arg Asn Ala Lys Val	
465 470 475 480	
ctg gtg gcc ggc aag agc gcc aac agc ctc gag aac cag acc ggc ggc	1488
Leu Val Ala Gly Lys Ser Ala Asn Ser Leu Glu Asn Gln Thr Gly Gly	
485 490 495	
tgg tcg ctc agc tgg caa ggc acc ggc aac gcc aac gcc gat ttc ggc	1536
Trp Ser Leu Ser Trp Gln Gly Thr Gly Asn Ala Asn Ala Asp Phe Gly	
500 505 510	
ggc ggc acg acc gtg tgg cag gcg atc cag aag atc gcc ccg aat gcc	1584
Gly Gly Thr Thr Val Trp Gln Ala Ile Gln Lys Ile Ala Pro Asn Ala	
515 520 525	
gaa ctc gac acc agc gcc gac ggc gcc aag ggc agc gat gcc tac gac	1632
Glu Leu Asp Thr Ser Ala Asp Gly Ala Lys Gly Ser Asp Ala Tyr Asp	
530 535 540	
gcc gcg atc gtc gtg atc ggt gaa aca ccg tac gcc gaa ggt gtc gga	1680
Ala Ala Ile Val Val Ile Gly Glu Thr Pro Tyr Ala Glu Gly Val Gly	
545 550 555 560	
gac atc ggc cgc agc aag acg ctg gaa ctc acc aag ctg cgt cca gaa	1728
Asp Ile Gly Arg Ser Lys Thr Leu Glu Leu Thr Lys Leu Arg Pro Glu	
565 570 575	

gac ctc gcc gtg atc gaa ggc ctg cgc gcc aag ggc gtg aag aaa atc Asp Leu Ala Val Ile Glu Gly Leu Arg Ala Lys Gly Val Lys Lys Ile 580 585 590	1776
gtc acg ctg ctg gtc tcc ggc cgc ccg ctc tac gtc aac aag gag ctg Val Thr Leu Leu Val Ser Gly Arg Pro Leu Tyr Val Asn Lys Glu Leu 595 600 605	1824
aac cgc tcg gac gcc ttc gtg gcg gcg tgg ctg ccc ggc acc gaa ggc Asn Arg Ser Asp Ala Phe Val Ala Ala Trp Leu Pro Gly Thr Glu Gly 610 615 620	1872
gac ggc gtc gcc gac gtg ctg ttc cgt gcg gcc gac ggc agc gtc gcg Asp Gly Val Ala Asp Val Leu Phe Arg Ala Ala Asp Gly Ser Val Ala 625 630 635 640	1920
cat ggc ttc agc ggc aag ctg tcg ttc tcg tgg ccg aag tcg gcc tgc His Gly Phe Ser Gly Lys Leu Ser Phe Ser Trp Pro Lys Ser Ala Cys 645 650 655	1968
cag acg ccg ctc aac cgt ggc gac gcc acc tac gac ccg ctc tac gct Gln Thr Pro Leu Asn Arg Gly Asp Ala Thr Tyr Asp Pro Leu Tyr Ala 660 665 670	2016
tat ggc tac ggc ctt caa tac ggc gag gag acc gat cag agc gcg tac Tyr Gly Tyr Gly Leu Gln Tyr Gly Glu Glu Thr Asp Gln Ser Ala Tyr 675 680 685	2064
gac gaa agc agt gcc acg gtc ggc tgc ggc atc cag gac ggc ggc ggc Asp Glu Ser Ser Ala Thr Val Gly Cys Gly Ile Gln Asp Gly Gly Gly 690 695 700	2112
acc acg gcc gag ccg ctg gcg gtg ttc gaa ggc gga gcc aac cag ggc Thr Thr Ala Glu Pro Leu Ala Val Phe Glu Gly Gly Ala Asn Gln Gly 705 710 715 720	2160
aac tgg aag ctg cgc atc ggc gcc gag tcg agc tgg agc aac gat gtg Asn Trp Lys Leu Arg Ile Gly Ala Glu Ser Trp Ser Asn Asp Val 725 730 735	2208
acg ctg gcc agc agc gcg gtg acg tcg acg ccg tcc aac gaa ctg cag Thr Leu Ala Ser Ser Ala Val Thr Ser Thr Pro Ser Asn Glu Leu Gln 740 745 750	2256
gcc gtg ccg gtg gac gac aag gcc ggg ccg caa tgg gcg gcg gtg aag Ala Val Pro Val Asp Asp Lys Ala Gly Arg Gln Trp Ala Ala Val Lys 755 760 765	2304
gcg acc tgg aac gac aag ccc ggc cag ctc tac atg caa agc gcc aac Ala Thr Trp Asn Asp Lys Pro Gly Gln Leu Tyr Met Gln Ser Ala Asn 770 775 780	2352
ccc ggc gac ctg gtg gac ctg atg gcc tat cag aac tcc ggt ggc gcg Pro Gly Asp Leu Val Asp Leu Met Ala Tyr Gln Asn Ser Gly Gly Ala 785 790 795 800	2400
ctg gtg ttc gac ctg cgt gtc gtc agt gcg ccg acc gac ccg gtc aag Leu Val Phe Asp Leu Arg Val Val Ser Ala Pro Thr Asp Pro Val Lys 805 810 815	2448
ctg cgc gtc gat tgc ggc tgg ccc tgt ctg ggc gag atc gac gtc acc	2496

Leu Arg Val Asp Cys Gly Trp Pro Cys Leu Gly Glu Ile Asp Val Thr
 820 825 830
 agc gcc gtc aag gcc cag ccg gtc aac gcc tgg aag gaa gtg gcg gtg 2544
 Ser Ala Val Lys Ala Gln Pro Val Asn Ala Trp Lys Glu Val Ala Val
 835 840 845
 tcg ctg cag tgt ttc gcc gac gcc ggc acc gac ctg gcc atc gtc aac 2592
 Ser Leu Gln Cys Phe Ala Asp Ala Gly Thr Asp Leu Ala Ile Val Asn
 850 855 860
 acg ccc ttc ctg atg tac acg tct ggc cgc ttc gaa gct gcc gtc gcg 2640
 Thr Pro Phe Leu Met Tyr Thr Ser Gly Arg Phe Glu Ala Ala Val Ala
 865 870 875 880
 aac atc cgt tgg gag ccc aag cgc acg ccc aac gtg ggg tgc aac ggc 2688
 Asn Ile Arg Trp Glu Pro Lys Arg Thr Pro Asn Val Gly Cys Asn Gly
 885 890 895
 gca ccg atc gcc gcc gcg cct tga 2712
 Ala Pro Ile Ala Ala Ala Pro *
 900

<210> 44
 <211> 903
 <212> PRT
 <213> Polyangium brachysporum

<400> 44
 Met Phe Leu His Pro Arg Gly Arg Met Thr Arg Leu Ala Leu Gly Cys
 1 5 10 15
 Ala Val Leu Cys Leu Ala Val Ala Gly Cys Gly Gly Gly Asp Asp Asp
 20 25 30
 Gly Asp Asp Asn Gly Thr Ala Pro Gln Pro Ala Pro Gly Gln Pro Glu
 35 40 45
 Pro Pro Thr Asp Thr Val Leu Lys Asp Trp Pro Arg Ile Asn Ser Ser
 50 55 60
 Ile Thr Ala Asp Ala Ala Ile Glu Ser Arg Val Asn Ser Leu Val Ala
 65 70 75 80
 Ala Met Thr Leu Glu Glu Lys Val Gly Gln Met Thr Gln Val Glu Ile
 85 90 95
 Gln Glu Val Thr Pro Glu Glu Ile Arg Gln Tyr His Ile Gly Ser Val
 100 105 110
 Leu Asn Gly Gly Gly Ser Phe Pro Lys Gln Asp Lys Gly Ala Ala Val
 115 120 125
 Thr Asp Trp Leu Ala Val Ala Asp Ala Leu Trp Ala Ala Ser Met Asp
 130 135 140
 Pro Ala Lys Pro Arg Arg Ile Pro Leu Ile Trp Gly Thr Asp Ala Val
 145 150 155 160
 His Gly His Asn Asn Val Lys Gly Ala Thr Ile Phe Pro His Asn Ile
 165 170 175
 Gly Leu Gly Ala Ala Arg Asp Pro Asp Leu Val Ala Arg Ile Gly Ala
 180 185 190
 Ala Thr Ala Leu Glu Val Ala Arg Thr Gly Ile Asp Trp Val Phe Ala
 195 200 205
 Pro Thr Leu Ala Val Val Arg Asp Asp Arg Trp Gly Arg Ser Tyr Glu
 210 215 220
 Gly Tyr Ser Glu Asp Pro Glu Ile Val Val Ser Tyr Ala Gly Lys Met
 225 230 235 240
 Val Glu Gly Leu Gln Gly Arg Leu Ala Gln Asp Ala Lys Ala Asn Glu

Lys	Val	Val	Ala	Thr	Ala	Lys	His	Phe	Val	Gly	Asp	Gly	Gly	Thr	Asp
			260					265						270	
Gln	Gly	Lys	Asp	Gln	Gly	Val	Thr	Arg	Val	Thr	Glu	Arg	Asp	Leu	Leu
		275						280					285		
Asn	Val	His	Ala	Arg	Gly	Tyr	Ile	Pro	Ala	Leu	Glu	Ala	Gly	Ala	Gln
	290					295					300				
Thr	Val	Met	Ala	Ser	Phe	Asn	Ser	Trp	Gln	Asp	Pro	Ser	Gln	Gly	Glu
305					310					315				320	
Gly	Ala	Lys	Ala	Phe	Lys	Met	His	Gly	Ser	Arg	Tyr	Leu	Leu	Thr	Glu
				325					330					335	
Ala	Leu	Lys	Gln	Lys	Met	Gly	Phe	Asp	Gly	Phe	Val	Val	Ser	Asp	Trp
			340					345					350		
Asn	Gly	Ile	Gly	Gln	Val	Thr	Thr	Glu	Asn	Ser	Asn	Ala	Thr	Arg	Asn
	355						360					365			
Cys	Ser	Asn	Ser	Asp	Cys	Pro	Glu	Ala	Ile	Asn	Ala	Gly	Ile	Asp	Met
	370				375						380				
Val	Met	Val	Pro	Tyr	Arg	Ala	Asp	Trp	Lys	Ala	Phe	Ile	Thr	Asn	Thr
385					390					395					400
Ile	Ala	Ile	Val	Arg	Lys	Gly	Glu	Ile	Ala	Gln	Glu	Arg	Ile	Asp	Asn
				405					410					415	
Ala	Val	Arg	Arg	Ile	Leu	Arg	Val	Lys	Leu	Arg	Ala	Gly	Leu	Phe	Asp
			420					425					430		
Lys	Pro	Thr	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Arg	Glu	Val	Gly	Ser	Ala
		435					440					445			
Glu	His	Arg	Ala	Leu	Ala	Arg	Glu	Ala	Val	Arg	Lys	Ser	Leu	Val	Leu
	450					455					460				
Leu	Lys	Asn	Asn	Gly	Arg	Val	Leu	Pro	Leu	Ala	Arg	Asn	Ala	Lys	Val
465					470					475					480
Leu	Val	Ala	Gly	Lys	Ser	Ala	Asn	Ser	Leu	Glu	Asn	Gln	Thr	Gly	Gly
				485					490					495	
Trp	Ser	Leu	Ser	Trp	Gln	Gly	Thr	Gly	Asn	Ala	Asn	Ala	Asp	Phe	Gly
			500					505					510		
Gly	Gly	Thr	Thr	Val	Trp	Gln	Ala	Ile	Gln	Lys	Ile	Ala	Pro	Asn	Ala
		515					520					525			
Glu	Leu	Asp	Thr	Ser	Ala	Asp	Gly	Ala	Lys	Gly	Ser	Asp	Ala	Tyr	Asp
	530					535					540				
Ala	Ala	Ile	Val	Val	Ile	Gly	Glu	Thr	Pro	Tyr	Ala	Glu	Gly	Val	Gly
545					550					555					560
Asp	Ile	Gly	Arg	Ser	Lys	Thr	Leu	Glu	Leu	Thr	Lys	Leu	Arg	Pro	Glu
				565					570					575	
Asp	Leu	Ala	Val	Ile	Glu	Gly	Leu	Arg	Ala	Lys	Gly	Val	Lys	Lys	Ile
			580					585					590		
Val	Thr	Leu	Leu	Val	Ser	Gly	Arg	Pro	Leu	Tyr	Val	Asn	Lys	Glu	Leu
	595					600						605			
Asn	Arg	Ser	Asp	Ala	Phe	Val	Ala	Ala	Trp	Leu	Pro	Gly	Thr	Glu	Gly
	610				615						620				
Asp	Gly	Val	Ala	Asp	Val	Leu	Phe	Arg	Ala	Ala	Asp	Gly	Ser	Val	Ala
625					630					635					640
His	Gly	Phe	Ser	Gly	Lys	Leu	Ser	Phe	Ser	Trp	Pro	Lys	Ser	Ala	Cys
				645					650					655	
Gln	Thr	Pro	Leu	Asn	Arg	Gly	Asp	Ala	Thr	Tyr	Asp	Pro	Leu	Tyr	Ala
			660					665					670		
Tyr	Gly	Tyr	Gly	Leu	Gln	Tyr	Gly	Glu	Glu	Thr	Asp	Gln	Ser	Ala	Tyr
	675					680						685			
Asp	Glu	Ser	Ser	Ala	Thr	Val	Gly	Cys	Gly	Ile	Gln	Asp	Gly	Gly	Gly
	690					695					700				
Thr	Thr	Ala	Glu	Pro	Leu	Ala	Val	Phe	Glu	Gly	Gly	Ala	Asn	Gln	Gly
705					710					715					720
Asn	Trp	Lys	Leu	Arg	Ile	Gly	Ala	Glu	Ser	Ser	Trp	Ser	Asn	Asp	Val
				725					730					735	

Thr Leu Ala Ser Ser Ala Val Thr Ser Thr Pro Ser Asn Glu Leu Gln
 740 745 750
 Ala Val Pro Val Asp Asp Lys Ala Gly Arg Gln Trp Ala Ala Val Lys
 755 760 765
 Ala Thr Trp Asn Asp Lys Pro Gly Gln Leu Tyr Met Gln Ser Ala Asn
 770 775 780
 Pro Gly Asp Leu Val Asp Leu Met Ala Tyr Gln Asn Ser Gly Gly Ala
 785 790 795 800
 Leu Val Phe Asp Leu Arg Val Val Ser Ala Pro Thr Asp Pro Val Lys
 805 810 815
 Leu Arg Val Asp Cys Gly Trp Pro Cys Leu Gly Glu Ile Asp Val Thr
 820 825 830
 Ser Ala Val Lys Ala Gln Pro Val Asn Ala Trp Lys Glu Val Ala Val
 835 840 845
 Ser Leu Gln Cys Phe Ala Asp Ala Gly Thr Asp Leu Ala Ile Val Asn
 850 855 860
 Thr Pro Phe Leu Met Tyr Thr Ser Gly Arg Phe Glu Ala Ala Val Ala
 865 870 875 880
 Asn Ile Arg Trp Glu Pro Lys Arg Thr Pro Asn Val Gly Cys Asn Gly
 885 890 895
 Ala Pro Ile Ala Ala Ala Pro
 900

<210> 45
 <211> 960
 <212> DNA
 <213> *Pyrococcus furiosus*

<220>
 <221> CDS
 <222> (1)...(960)
 <223> clone # 7EG1

<400> 45
 atg agc aag aaa aag ttc gtc atc gta tct atc tta aca atc ctt tta 48
 Met Ser Lys Lys Lys Phe Val Ile Val Ser Ile Leu Thr Ile Leu Leu
 1 5 10 15

 gta cag gca ata tat ttt gta gaa aag tat cat acc tct gag gac aag 96
 Val Gln Ala Ile Tyr Phe Val Glu Lys Tyr His Thr Ser Glu Asp Lys
 20 25 30

 tca act tca aat acc tca tct aca cca ccc caa aca aca ctt tcc act 144
 Ser Thr Ser Ser Asn Thr Ser Ser Thr Pro Pro Gln Thr Thr Leu Ser Thr
 35 40 45

 acc aag gtt ctc aag att aga tac cct gat gac ggt gag tgg cca gga 192
 Thr Lys Val Leu Lys Ile Arg Tyr Pro Asp Asp Gly Glu Trp Pro Gly
 50 55 60

 gct cct att gat aag gat ggt gat ggg aac cca gaa ttc tac att gaa 240
 Ala Pro Ile Asp Lys Asp Gly Asp Gly Asn Pro Glu Phe Tyr Ile Glu
 65 70 75 80

 ata aac cta tgg aac att ctt aat gct act gga ttt gct gag atg acg 288
 Ile Asn Leu Trp Asn Ile Leu Asn Ala Thr Gly Phe Ala Glu Met Thr
 85 90 95

 tac aat tta acc agc ggc gtc ctt cac tac gtc caa caa ctt gac aac 336
 Tyr Asn Leu Thr Ser Gly Val Leu His Tyr Val Gln Gln Leu Asp Asn
 100 105 110

att gtc ttg agg gat aga agt aat tgg gtg cat gga tac ccc gaa ata Ile Val Leu Arg Asp Arg Ser Asn Trp Val His Gly Tyr Pro Glu Ile 115 120 125	384
ttc tat gga aac aag cca tgg aat gca aac tac gca act gat ggc cca Phe Tyr Gly Asn Lys Pro Trp Asn Ala Asn Tyr Ala Thr Asp Gly Pro 130 135 140	432
ata cca tta ccc agt aaa gtt tca aac cta aca gac ttc tat cta aca Ile Pro Leu Pro Ser Lys Val Ser Asn Leu Thr Asp Phe Tyr Leu Thr 145 150 155 160	480
atc tcc tat aaa ctt gag ccc aag aac ggc ctg cca att aac ttc gca Ile Ser Tyr Lys Leu Glu Pro Lys Asn Gly Leu Pro Ile Asn Phe Ala 165 170 175	528
ata gaa tcc tgg tta acg aga gaa gct tgg aga aca aca gga att aac Ile Glu Ser Trp Leu Thr Arg Glu Ala Trp Arg Thr Thr Gly Ile Asn 180 185 190	576
agc gat gag caa gaa gta atg ata tgg att tac tat gac gga tta caa Ser Asp Glu Gln Glu Val Met Ile Trp Ile Tyr Tyr Asp Gly Leu Gln 195 200 205	624
ccg gct ggc tcc aaa gtt aag gag att gta gtc cca ata ata gtt aac Pro Ala Gly Ser Lys Val Lys Glu Ile Val Val Pro Ile Ile Val Asn 210 215 220	672
gga aca cca gta aat gct aca ttt gaa gta tgg aag gca aac att ggt Gly Thr Pro Val Asn Ala Thr Phe Glu Val Trp Lys Ala Asn Ile Gly 225 230 235 240	720
tggt gag tat gtt gca ttt aga ata aag acc cca atc aaa gag gga aca Trp Glu Tyr Val Ala Phe Arg Ile Lys Thr Pro Ile Lys Glu Gly Thr 245 250 255	768
gtg aca att cca tac gga gca ttt ata agt gtt gca gcc aac att tca Val Thr Ile Pro Tyr Gly Ala Phe Ile Ser Val Ala Ala Asn Ile Ser 260 265 270	816
agc tta cca aat tac aca gaa ctt tac tta gag gac gtg gag att gga Ser Leu Pro Asn Tyr Thr Glu Leu Tyr Leu Glu Asp Val Glu Ile Gly 275 280 285	864
act gag ttt gga acg cca agc act acc tcc gcc cac cta gag tgg tgg Thr Glu Phe Gly Thr Pro Ser Thr Thr Ser Ala His Leu Glu Trp Trp 290 295 300	912
atc aca aac ata aca cta act cct cta gat aga cct ctt att tcc taa Ile Thr Asn Ile Thr Leu Thr Pro Leu Asp Arg Pro Leu Ile Ser * 305 310 315	960

<210> 46

<211> 319

<212> PRT

<213> *Pyrococcus furiosus*

<400> 46

Met Ser Lys Lys Lys Phe Val Ile Val Ser Ile Leu Thr Ile Leu Leu

1	5	10	15
Val Gln Ala Ile Tyr Phe Val Glu Lys Tyr His Thr Ser Glu Asp Lys			
	20	25	30
Ser Thr Ser Asn Thr Ser Ser Thr Pro Pro Gln Thr Thr Leu Ser Thr			
	35	40	45
Thr Lys Val Leu Lys Ile Arg Tyr Pro Asp Asp Gly Glu Trp Pro Gly			
	50	55	60
Ala Pro Ile Asp Lys Asp Gly Asp Gly Asn Pro Glu Phe Tyr Ile Glu			
65	70	75	80
Ile Asn Leu Trp Asn Ile Leu Asn Ala Thr Gly Phe Ala Glu Met Thr			
	85	90	95
Tyr Asn Leu Thr Ser Gly Val Leu His Tyr Val Gln Gln Leu Asp Asn			
	100	105	110
Ile Val Leu Arg Asp Arg Ser Asn Trp Val His Gly Tyr Pro Glu Ile			
	115	120	125
Phe Tyr Gly Asn Lys Pro Trp Asn Ala Asn Tyr Ala Thr Asp Gly Pro			
	130	135	140
Ile Pro Leu Pro Ser Lys Val Ser Asn Leu Thr Asp Phe Tyr Leu Thr			
145	150	155	160
Ile Ser Tyr Lys Leu Glu Pro Lys Asn Gly Leu Pro Ile Asn Phe Ala			
	165	170	175
Ile Glu Ser Trp Leu Thr Arg Glu Ala Trp Arg Thr Thr Gly Ile Asn			
	180	185	190
Ser Asp Glu Gln Glu Val Met Ile Trp Ile Tyr Tyr Asp Gly Leu Gln			
	195	200	205
Pro Ala Gly Ser Lys Val Lys Glu Ile Val Val Pro Ile Ile Val Asn			
	210	215	220
Gly Thr Pro Val Asn Ala Thr Phe Glu Val Trp Lys Ala Asn Ile Gly			
225	230	235	240
Trp Glu Tyr Val Ala Phe Arg Ile Lys Thr Pro Ile Lys Glu Gly Thr			
	245	250	255
Val Thr Ile Pro Tyr Gly Ala Phe Ile Ser Val Ala Ala Asn Ile Ser			
	260	265	270
Ser Leu Pro Asn Tyr Thr Glu Leu Tyr Leu Glu Asp Val Glu Ile Gly			
	275	280	285
Thr Glu Phe Gly Thr Pro Ser Thr Thr Ser Ala His Leu Glu Trp Trp			
	290	295	300
Ile Thr Asn Ile Thr Leu Thr Pro Leu Asp Arg Pro Leu Ile Ser			
305	310	315	

<210> 47
 <211> 1515
 <212> DNA
 <213> Vibrio harveyi

<220>
 <221> CDS
 <222> (1)...(1515)
 <223> clone # 91GP2

<400> 47	
atg aga ggt aac acg atg aag caa aaa gcg cta tat cga gca gta gca	48
Met Arg Gly Asn Thr Met Lys Gln Lys Ala Leu Tyr Arg Ala Val Ala	
1 5 10 15	
atg ggt ttg agt ggt ctt gcg aac gtc gca tcc gct aat gag atg gta	96
Met Gly Leu Ser Gly Leu Ala Asn Val Ala Ser Ala Asn Glu Met Val	
20 25 30	
aat cct gat ggt ggt gtc gta gtg ggt tac tgg cat aac tgg tgc gat	144
Asn Pro Asp Gly Gly Val Val Val Gly Tyr Trp His Asn Trp Cys Asp	

35	40	45	
ggc gct ggt tac aag gga ggt aat gca ccg tgt gta aca ttg gat gaa			192
Gly Ala Gly Tyr Lys Gly Gly Asn Ala Pro Cys Val Thr Leu Asp Glu			
50	55	60	
ggt gat cct atg tac aat gtg gtt aac gtc tcc ttt atg aag gta ttc			240
Val Asp Pro Met Tyr Asn Val Val Asn Val Ser Phe Met Lys Val Phe			
65	70	75	80
aat acc agt gaa ggt cgt att cca acc ttt aag ctc gat cca aat atc			288
Asn Thr Ser Glu Gly Arg Ile Pro Thr Phe Lys Leu Asp Pro Asn Ile			
	85	90	95
ggc ctt tca gaa caa caa ttt ttt gac caa att gaa gct cta aac caa			336
Gly Leu Ser Glu Gln Gln Phe Phe Asp Gln Ile Glu Ala Leu Asn Gln			
	100	105	110
caa gga cgt gcc gtt ctc atc gct ctt ggt ggc gca gat gct cac gtt			384
Gln Gly Arg Ala Val Leu Ile Ala Leu Gly Gly Ala Asp Ala His Val			
	115	120	125
gaa ctt aga act ggt gac gaa caa gcg ttc gca caa gag att att cgt			432
Glu Leu Arg Thr Gly Asp Glu Gln Ala Phe Ala Gln Glu Ile Ile Arg			
	130	135	140
tta acg gat aag ttc ggt ttt gat ggt cta gat atc gat tta gag cag			480
Leu Thr Asp Lys Phe Phe Asp Gly Leu Asp Ile Asp Leu Glu Gln			
145	150	155	160
tca gca gta acg gca gag aac aac caa acc gta att cca gct gca ctt			528
Ser Ala Val Thr Ala Glu Asn Asn Gln Thr Val Ile Pro Ala Ala Leu			
	165	170	175
cgc ctt gta aaa gag cat tat caa caa caa ggt aag aac ttc cta att			576
Arg Leu Val Lys Glu His Tyr Gln Gln Gln Gly Lys Asn Phe Leu Ile			
	180	185	190
acg atg gcg cct gaa ttc cct tat cta aca gaa ggt ggc aag tat gtt			624
Thr Met Ala Pro Glu Phe Pro Tyr Leu Thr Glu Gly Gly Lys Tyr Val			
	195	200	205
cct tac att act ggt tta gaa ggg tac tac gat tgg atc aac cct cag			672
Pro Tyr Ile Thr Gly Leu Glu Gly Tyr Tyr Asp Trp Ile Asn Pro Gln			
	210	215	220
ttt tac aat caa ggt ggt gac ggt att tgg gtt gat ggc gtg ggt tgg			720
Phe Tyr Asn Gln Gly Gly Asp Gly Ile Trp Val Asp Gly Val Gly Trp			
225	230	235	240
ata gcg caa aac aat gat gag tta aaa caa gag ttt att tac tac att			768
Ile Ala Gln Asn Asn Asp Glu Leu Lys Gln Glu Phe Ile Tyr Tyr Ile			
	245	250	255
tcg gac gct cta tcg aac ggt aca cgc ggt ttc cac aaa atc ccg cat			816
Ser Asp Ala Leu Ser Asn Gly Thr Arg Gly Phe His Lys Ile Pro His			
	260	265	270
gac aaa ctg gtg ttt ggt atc cca tct aac att gat gct gct gca acg			864
Asp Lys Leu Val Phe Gly Ile Pro Ser Asn Ile Asp Ala Ala Ala Thr			
	275	280	285

ggc ttt gtt caa aac cct caa gac ctt tac gac gcg ttt gat caa ctt Gly Phe Val Gln Asn Pro Gln Asp Leu Tyr Asp Ala Phe Asp Gln Leu 290 295 300	912
aaa gcg caa ggg cag gca ctt cgt ggc gta atg aca tgg tcg gtg aac Lys Ala Gln Gly Gln Ala Leu Arg Gly Val Met Thr Trp Ser Val Asn 305 310 315 320	960
tgg gat atg ggc acc gat aaa aat ggc caa gcg tac ggt gaa aaa ttc Trp Asp Met Gly Thr Asp Lys Asn Gly Gln Ala Tyr Gly Glu Lys Phe 325 330 335	1008
gtg aag gat tac ggt ccg ttt atc cac ggg cag act cca cca cca agt Val Lys Asp Tyr Gly Pro Phe Ile His Gly Gln Thr Pro Pro Pro Ser 340 345 350	1056
gaa ggt gaa cca gtt ttt agt ggc ctc aac gat gtt cgt gtg cat cac Glu Gly Glu Pro Val Phe Ser Gly Leu Asn Asp Val Arg Val His His 355 360 365	1104
ggg agt tca ttt gac ccg tat gca ggt gtt act gcg tct gat aaa gaa Gly Ser Ser Phe Asp Pro Tyr Ala Gly Val Thr Ala Ser Asp Lys Glu 370 375 380	1152
gat gga gac cta acc aac agc atc act gtc gaa ggt tca gtt gat gtg Asp Gly Asp Leu Thr Asn Ser Ile Thr Val Glu Gly Ser Val Asp Val 385 390 395 400	1200
aac acg gta ggc aca tat gtt ttg gtt tac agt gta aaa gac agc gac Asn Thr Val Gly Thr Tyr Val Leu Val Tyr Ser Val Lys Asp Ser Asp 405 410 415	1248
aac aat gaa acc aag caa agt aga acg gtt gtt gtt tac agc cta gtg Asn Asn Glu Thr Lys Gln Ser Arg Thr Val Val Val Tyr Ser Leu Val 420 425 430	1296
cct gag ttt gaa ggt gtc gca gat acg acc atc cag ctt ggt gac gct Pro Glu Phe Glu Gly Val Ala Asp Thr Thr Ile Gln Leu Gly Asp Ala 435 440 445	1344
ttt gac cca atg gca ggc gta aaa gcg acg gat gca gaa gac ggt gat Phe Asp Pro Met Ala Gly Val Lys Ala Thr Asp Ala Glu Asp Gly Asp 450 455 460	1392
ttg act gat cgg tat cta cgc cgc cta agg tca ctt ctg cgg tgc gat Leu Thr Asp Arg Tyr Leu Arg Arg Leu Arg Ser Leu Leu Arg Cys Asp 465 470 475 480	1440
agc ctt ctg tgc cat ttg gtg caa ccg ccc agt ttt cca gac gct caa Ser Leu Leu Cys His Leu Val Gln Pro Pro Ser Phe Pro Asp Ala Gln 485 490 495	1488
cga tgg ttg cca tct ctt tct ggt tga Arg Trp Leu Pro Ser Leu Ser Gly *	1515
500	

<210> 48
 <211> 504
 <212> PRT

<213> *Vibrio harveyi*

<400> 48

Met	Arg	Gly	Asn	Thr	Met	Lys	Gln	Lys	Ala	Leu	Tyr	Arg	Ala	Val	Ala
1			5					10						15	
Met	Gly	Leu	Ser	Gly	Leu	Ala	Asn	Val	Ala	Ser	Ala	Asn	Glu	Met	Val
		20					25					30			
Asn	Pro	Asp	Gly	Gly	Val	Val	Val	Gly	Tyr	Trp	His	Asn	Trp	Cys	Asp
	35						40				45				
Gly	Ala	Gly	Tyr	Lys	Gly	Gly	Asn	Ala	Pro	Cys	Val	Thr	Leu	Asp	Glu
	50				55						60				
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Ser	Ala	Val	Thr	Ala	Glu	Asn	Asn	Gln	Thr	Val	Ile	Pro	Ala	Ala	Leu
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Arg	Leu	Val	Lys	Glu	His	Tyr	Gln	Gln	Gly	Lys	Asn	Phe	Leu	Ile	
		180					185					190			
Thr	Met	Ala	Pro	Glu	Phe	Pro	Tyr	Leu	Thr	Glu	Gly	Gly	Lys	Tyr	Val
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Pro	Tyr	Ile	Thr	Gly	Leu	Glu	Gly	Tyr	Tyr	Asp	Trp	Ile	Asn	Pro	Gln
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Phe	Tyr	Asn	Gln	Gly	Gly	Asp	Gly	Ile	Trp	Val	Asp	Gly	Val	Gly	Trp
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Ser	Asp	Ala	Leu	Ser	Asn	Gly	Thr	Arg	Gly	Phe	His	Lys	Ile	Pro	His
		260					265					270			
Asp	Lys	Leu	Val	Phe	Gly	Ile	Pro	Ser	Asn	Ile	Asp	Ala	Ala	Ala	Thr
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Gly	Phe	Val	Gln	Asn	Pro	Gln	Asp	Leu	Tyr	Asp	Ala	Phe	Asp	Gln	Leu
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Lys	Ala	Gln	Gly	Gln	Ala	Leu	Arg	Gly	Val	Met	Thr	Trp	Ser	Val	Asn
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Trp	Asp	Met	Gly	Thr	Asp	Lys	Asn	Gly	Gln	Ala	Tyr	Gly	Glu	Lys	Phe
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Pro	Glu	Phe	Glu	Gly	Val	Ala	Asp	Thr	Thr	Ile	Gln	Leu	Gly	Asp	Ala
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